STIC Search Report
Biotech-Chem Library

USPTO — Scientific & Technical Information Center

TO: Chun Crowder
Location: REM-3B59/3C70
Art Unit: 1644
Thursday, February 16, 2006
Case Serial Number: 10/524134

From: Toby Port
Location: Biotech-Chem Library
          REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Crowder,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

sira
Search and Information
Resources Administration

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: February 15, 2006, 17:53:06 ; Search time 10.3246 Seconds
                 (without alignments)
                 147.285 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILLTQSPAILSVSPGERVS.........CQQSNTWPFTFGGGTKLEIK 107

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA_New:*
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                 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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                 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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                 Minimum DB seq length: 0
                 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	107	7	US-10-524-134-4	Sequence 26, Appl
2	557	100.0	107	7	US-11-108-135-26	Sequence 26, Appl
3	499	89.6	107	7	US-11-126-978-26	Sequence 26, App
4	484	86.9	107	7	US-11-004-590-234	Sequence 234, App
5	484	86.9	107	7	US-11-010-954-3	Sequence 3, Appl
6	484	86.9	107	7	US-11-053-750-3	Sequence 3, Appli
7	484	86.9	107	7	US-11-053-749-3	Sequence 3, Appli
8	484	86.9	107	7	US-11-170-753-3	Sequence 3, Appli
9	484	86.9	107	7	US-11-179-359-3	Sequence 3, Appli
10	484	86.9	107	7	US-11-181-030-3	Sequence 3, Appl
11	484	86.9	107	7	US-11-182-033-3	Sequence 3, Appli
12	484	86.9	107	7	US-11-195-589-3	Sequence 3, Appl
13	484	86.9	117	7	US-11-005-726-10	Sequence 10, Appl
14	484	86.9	109	7	US-11-005-726-12	Sequence 12, Appl
15	484	86.9	214	7	US-11-183-205-42	Sequence 42, Appli
16	447	80.3	226	7	US-11-183-205-163	Sequence 163, Appl
17	445	79.9	108	7	US-11-108-135-18	Sequence 18, Appli
18	445	79.9	107	7	US-11-126-978-18	Sequence 18, Appl
19	440	79.0	107	7	US-11-004-590-379	Sequence 379, Appl
20	437	78.5	107	7	US-11-108-135-20	Sequence 20, Appl
21	437	78.5	107	7	US-11-004-590-251	Sequence 251, App
22	437	78.5	107	7	US-11-004-590-259	Sequence 259, App
23	437	78.5	107	7	US-11-004-590-324	Sequence 324, App
24	437	78.5	107	7	US-11-004-590-381	Sequence 381, App
25	437	78.5	107	7	US-11-126-978-20	Sequence 20, Appl
26	436	78.3	107	7	US-11-004-590-250	Sequence 250, App
27	436	78.3	107	7	US-11-004-590-257	Sequence 257, App
28	436	78.3	107	7	US-11-004-590-260	Sequence 260, App
29	436	78.3	107	7	US-11-004-590-323	Sequence 323, App
30	435	78.1	107	7	US-11-004-590-248	Sequence 248, App
31	435	78.1	108	7	US-11-004-590-255	Sequence 255, Appli
32	435	78.1	107	7	US-11-005-726-5	Sequence 5, Appli
33	434	77.9	107	7	US-11-004-590-246	Sequence 246, Appl
34	433	77.7	107	7	US-11-108-135-22	Sequence 22, Appl
35	433	77.7	107	7	US-11-004-590-258	Sequence 258, App
36	433	77.7	107	7	US-11-004-590-325	Sequence 325, Appl
37	433	77.6	107	7	US-11-126-978-22	Sequence 22, Appl
38	432	77.6	107	7	US-11-004-590-249	Sequence 249, Appl
39	432	77.6	107	7	US-11-004-590-254	Sequence 254, App
40	432	77.6	107	7	US-11-004-590-282	Sequence 282, App
41	432	77.6	107	7	US-11-004-590-312	Sequence 312, App
42	432	77.6	108	7	US-11-005-726-8	Sequence 8, Appli
43	431	77.4	107	7	US-11-004-590-245	Sequence 245, App
44	431	77.4	107	7	US-11-004-590-293	Sequence 293, App
45	431	77.4	107	7	US-11-004-590-303	Sequence 303, App

ALIGNMENTS

RESULT 1
US-11-108-135-26
Sequence 26, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuaillon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/582,804
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse 2B6 light chain variable region
US-11-108-135-26

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Best Local Similarity 100.0%;   Pred. No. 8.2e-39;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db  61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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RESULT 2
US-11-126-978-26

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Sequence 26, Application US/11126978
Publication No. US20060013810A1
GENERAL INFORMATION:
  APPLICANT: Johnson, Leslie Sydnor
  APPLICANT: Huang, Ling
  TITLE OF INVENTION: HUMANIZED FcgammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THER
  CURRENT APPLICATION NUMBER: US/11,126,978
  CURRENT FILING DATE: 2005-05-10
  PRIOR APPLICATION NUMBER: 60/582,043
  PRIOR FILING DATE: 2004-06-21
  PRIOR APPLICATION NUMBER: 60/569,882
  PRIOR FILING DATE: 2004-05-10
  NUMBER OF SEQ ID NOS: 58
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 26
  LENGTH: 107
  TYPE: PRT
  ORGANISM: mus sp.
  FEATURE:
  OTHER INFORMATION: Mouse 2B6 light chain variable region
US-11-126-978-26

  Query Match             100.0%;  Score 557;  DB 7;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-39;  Mismatches 0;  Indels 0;  Gaps 0;
  Matches  107;  Conservative  0;

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Db 61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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RESULT 3
US-11-004-590-234
Sequence 234, Application US/11004590
Publication No. US20060008883A1
GENERAL INFORMATION:
  APPLICANT: Lazar, Gregory Alan
  APPLICANT: Desjarlais, John R.
  APPLICANT: Hammond, Phillip W.
  TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
  FILE REFERENCE: 185832/US/5
  CURRENT APPLICATION NUMBER: US/11/004,590
  CURRENT FILING DATE: 2004-12-03
  PRIOR APPLICATION NUMBER: US 60/527,167
  PRIOR FILING DATE: 2003-12-04
  PRIOR APPLICATION NUMBER: US 60/581,613
  PRIOR FILING DATE: 2004-06-21
  PRIOR APPLICATION NUMBER: US 60/601,665
  PRIOR FILING DATE: 2004-08-13
  PRIOR APPLICATION NUMBER: US 60/619,483
  PRIOR FILING DATE: 2004-10-14
  NUMBER OF SEQ ID NOS: 458
  SOFTWARE: Patentin version 3.3
  SEQ ID NO 234
  LENGTH: 107
  TYPE: PRT
  ORGANISM: Homo sapiens
US-11-004-590-234

  Query Match             89.6%;  Score 499;  DB 7;  Length 107;
  Best Local Similarity   89.7%;  Pred. No. 3.8e-34;  Mismatches 9;  Indels 0;  Gaps 0;
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Qy  1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
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Db  1 DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
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Qy 61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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Db 61 RFSGSGSGTDFTLSINSVESEDIADYYCQQNNWPFTFGAGTKLEIK 107
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RESULT 4
US-11-010-954-3
Sequence 3, Application US/11010954
Publication No. US20050249735A1
GENERAL INFORMATION:
  APPLICANT: Le, Junming
  APPLICANT: Vilcek, Jan
  APPLICANT: Daddona, Peter
  APPLICANT: Ghrayeb, John
  APPLICANT: Knight, David
  APPLICANT: Siegel, Scott
  APPLICANT: Shealy, David
  TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antib
  TITLE OF INVENTION: and Peptides of Human Tumor Necrosis Factor
  CURRENT APPLICATION NUMBER: US/11/010,954
  CURRENT FILING DATE: 2004-12-13
  PRIOR APPLICATION NUMBER: US 10/637,759
  PRIOR FILING DATE: 2003-08-08
  PRIOR APPLICATION NUMBER: US 09/920,137
  PRIOR FILING DATE: 2001-08-01
  PRIOR APPLICATION NUMBER: US 09/927,703
  PRIOR FILING DATE: 2001-08-10
  PRIOR APPLICATION NUMBER: US 09/756,398
  PRIOR FILING DATE: 2001-01-08
  PRIOR APPLICATION NUMBER: US 09/236,826
  PRIOR FILING DATE: 2000-09-29
  PRIOR APPLICATION NUMBER: US 60/223,360
  PRIOR FILING DATE: 2000-08-07
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 3
  LENGTH: 107
  TYPE: PRT
  ORGANISM: Mus Balb/c
US-11-010-954-3

  Query Match             86.9%;  Score 484;  DB 7;  Length 107;
  Best Local Similarity   85.0%;  Pred. No. 6e-33;  Mismatches 8;  Indels 0;  Gaps 0;
  Matches  91;  Conservative  8;

Qy  1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
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Db  1 DILLTQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60

Qy 61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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Db 61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
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RESULT 5
US-11-053-750-3
Sequence 3, Application US/11053750
Publication No. US20050255104A1
GENERAL INFORMATION:
  APPLICANT: Le, Junming
  APPLICANT: Vilcek, Jan
  APPLICANT: Daddona, Peter
  APPLICANT: Ghrayeb, John
  APPLICANT: Knight, David
  APPLICANT: Siegel, Scott
  APPLICANT: Scallon, Bernard
  TITLE OF INVENTION: Methods of Treating Psoriasis Using
  TITLE OF INVENTION: Anti-TNF Receptor Fusion Proteins
  FILE REFERENCE: 0975.1005-045
  CURRENT APPLICATION NUMBER: US/11/053,750
  CURRENT FILING DATE: 2005-02-07
  PRIOR APPLICATION NUMBER: U.S. 09/927,703
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OM protein - protein search, using sw model

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                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.
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Run on: February 15, 2006, 17:52:22 ; Search time 106.061 Seconds
                                                   (without alignments)
                                                   421.527 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILLTQSPAILSVSPGERVS..........CQQSNTWPFTFGGGTKLEIK 107

Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	557	100.0	107	4	US-10-643-857-4	Sequence 4, Appli
2	557	100.0	107	4	US-10-524-134-4	Sequence 4, Appli
3	504	90.5	107	5	US-10-923-068-507	Sequence 507, App
4	504	90.5	108	5	US-11-412-703A-129	Sequence 129, App
5	503	90.3	107	3	US-09-842-776A-58	Sequence 58, Appl
6	503	90.3	107	4	US-10-467-546-1	Sequence 1, Appli
7	503	90.3	107	4	US-10-666-332-1	Sequence 1, Appl
8	503	90.3	107	6	US-11-050-435-32	Sequence 32, Appli
9	503	90.3	111	6	US-11-050-435-6	Sequence 6, Appl
10	503	90.3	214	6	US-10-467-546-3	Sequence 3, Appli
11	503	90.3	214	5	US-10-666-332-3	Sequence 3, Appl
12	500	89.8	107	4	US-10-239-656-38	Sequence 38, Appl
13	500	89.8	510	4	US-10-239-656-49	Sequence 49, Appli
14	499	89.6	107	4	US-10-453-698-129	Sequence 129, App
15	499	89.6	107	4	US-10-308-817-129	Sequence 129, App
16	499	89.6	107	2	US-11-004-054-2	Sequence 2, Appli
17	499	89.6	107	5	US-10-374-600-5	Sequence 5, Appli
18	499	89.6	127	4	US-10-374-600-11	Sequence 11, Appl
19	499	89.6	127	4	US-10-374-600-15	Sequence 15, Appl
20	499	89.6	127	4	US-10-374-531-5	Sequence 5, Appl
21	499	89.6	127	4	US-10-374-531-11	Sequence 11, Appl
22	499	89.6	127	4	US-10-374-531-15	Sequence 15, Appl
23	499	89.6	236	5	US-10-728-723-18	Sequence 18, Appl
24	498	89.4	107	5	US-10-901-736-1	Sequence 1, Appl
25	498	89.4	242	4	US-10-336-210-9	Sequence 9, Appli
26	498	89.4	244	3	US-09-940-391-1	Sequence 1, Appli
27	498	89.4	244	4	US-10-336-210-8	Sequence 8, Appli
28	497	89.2	107	4	US-10-239-656-28	Sequence 28, Appl
29	497	89.2	510	4	US-10-239-656-48	Sequence 48, Appl
30	496	89.0	107	4	US-10-308-817-130	Sequence 130, App
31	496	89.0	107	4	US-10-453-698-130	Sequence 130, App
32	489	87.8	214	5	US-10-488-074-72	Sequence 72, Appl
33	488	87.6	214	5	US-10-488-074-68	Sequence 68, Appl
34	484	86.9	107	3	US-09-756-301A-3	Sequence 3, Appli
35	484	86.9	107	3	US-09-927-703-3	Sequence 3, Appli
36	484	86.9	107	3	US-09-766-535A-3	Sequence 3, Appli
37	484	86.9	107	3	US-09-756-161A-3	Sequence 3, Appli
38	484	86.9	107	3	US-09-756-398B-3	Sequence 3, Appli
39	484	86.9	107	3	US-09-897-724-3	Sequence 3, Appli
40	484	86.9	107	4	US-10-010-229-3	Sequence 3, Appli
41	484	86.9	107	3	US-10-043-450-3	Sequence 3, Appli
42	484	86.9	107	5	US-10-044-534-3	Sequence 3, Appli
43	484	86.9	107	4	US-10-043-432-3	Sequence 3, Appli
44	484	86.9	107	4	US-10-208-145-3	Sequence 3, Appli
45	484	86.9	107	4	US-10-198-845-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-10-643-857-4

; Sequence 4, Application US/10643857
; Publication No. US20040185045A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; TITLE OF INVENTION: Anti-FcgRIIB monoclonal antibodies and their use in enhancing
; TITLE OF INVENTION: immune response
; FILE REFERENCE: 11183-010-999
; CURRENT APPLICATION NUMBER: US/10/643,857
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,266
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-643-857-4

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  Matches  107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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RESULT 2
US-10-524-134-4

; Sequence 4, Application US/10524134
; Publication No. US20050215767A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; TITLE OF INVENTION: Anti-FcgRIIB monoclonal antibodies and their use in enhancing
; TITLE OF INVENTION: immune response
; FILE REFERENCE: 11183-003-999
; CURRENT APPLICATION NUMBER: US/10/524,134
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: PCT/US03/25399
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,266

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;  PRIOR FILING DATE: 2002-08-14
;  NUMBER OF SEQ ID NO: 4
;  SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
;  LENGTH: 107
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-524-134-4

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Db       Best Local Similarity  100.0%;  Pred. No. 1,6e-46;
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Qy  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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Db  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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RESULT 3
US-10-923-068-507
; Sequence 507, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 507
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-923-068-507

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Qy       Query Match     90.5%;  Score 504;  DB 5;  Length 107;
Db       Best Local Similarity  90.7%;  Pred. No. 2,3e-41;
         Matches 97;  Conservative  1;  Mismatches  9;  Indels  0;  Gaps  0;

Qy   1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
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Db   1  DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60

Qy  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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Db  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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RESULT 4
US-10-412-703A-129
; Sequence 129, Application US/10412703A
; Publication No. US20030219439A1
; GENERAL INFORMATION:
; APPLICANT: Reed et al.
; TITLE OF INVENTION: Recombinant Anti-Interleukin-9 Antibodies
; FILE REFERENCE: IL400US
; CURRENT APPLICATION NUMBER: 60/371,728
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/412,703A
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/371,683
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-703A-129

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Qy       Query Match     90.5%;  Score 504;  DB 4;  Length 108;
Db       Best Local Similarity  90.7%;  Pred. No. 2,3e-41;
         Matches 97;  Conservative  1;  Mismatches  9;  Indels  0;  Gaps  0;

Qy   1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
        |||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||
Db   1  DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60

Qy  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
        |||| ||||||||||||||||||||||||||||||: |||| || |:|
Db  61  RFSGGGSGTDFILSINSVESEDIADYYCQQSNNWPLTFGAGTKLELK 107
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RESULT 5
US-09-842-776A-58
; Sequence 58, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-842-776A-58

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Qy       Query Match     90.3%;  Score 503;  DB 3;  Length 107;
Db       Best Local Similarity  91.6%;  Pred. No. 2,9e-41;
         Matches 98;  Conservative  1;  Mismatches  8;  Indels  0;  Gaps  0;

Qy   1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
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Db   1  DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYGSESISGIPS 60

Qy  61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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Db  61  RFSGSGSGTDFSLSINSVESEDIADYYCQQSNTWPLTFGAGTKLELK 107
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RESULT 6
US-10-467-546-1
; Sequence 1, Application US/10467546
; Publication No. US20040096901A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: PCT/EP02/01420
; CURRENT APPLICATION NUMBER: US/10/467,546
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 15, 2006, 17:36:50 ; Search time 30.9737 seconds
(without alignments)
285.607 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILLTQSPAILSVSPGERVS........CQQSNTWPFTFGGGTKLEIK 107

Scoring table: BLOSUM62
Scoring: Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	498	89.4	107	1	US-08-476-176B-4	Sequence 4, Appli
2	498	89.4	107	1	US-08-127-721A-4	Sequence 4, Appli
3	498	89.4	107	2	US-08-485-246A-4	Sequence 4, Appli
4	498	89.4	244	2	US-09-244-369B-1	Sequence 1, Appli
5	494	88.7	244	2	US-07-956-399-2	Sequence 2, Appli
6	492	88.3	240	1	US-07-956-399-1	Sequence 1, Appli
7	491	88.2	107	1	US-08-232-081B-40	Sequence 40, Appl
8	487	87.4	239	1	US-07-956-399-4	Sequence 4, Appl
9	487	87.4	106	1	US-08-800-198-4	Sequence 4, Appli
10	487	87.4	106	2	US-09-296-595-4	Sequence 4, Appli
11	487	87.4	240	1	US-08-800-198-8	Sequence 8, Appli
12	484	86.9	240	2	US-09-296-595-8	Sequence 8, Appli
13	484	86.9	240	1	US-08-192-102-3	Sequence 3, Appli
14	484	86.9	107	1	US-08-324-799-3	Sequence 3, Appli
15	484	86.9	107	2	US-08-192-861A-3	Sequence 3, Appli
16	484	86.9	107	1	US-09-133-119-3	Sequence 3, Appli
17	484	86.9	107	2	US-08-192-093A-3	Sequence 3, Appli
18	484	86.9	107	1	US-09-756-301B-3	Sequence 3, Appli
19	484	86.9	107	2	US-09-756-398B-3	Sequence 3, Appli
20	480	86.2	143	1	US-08-653-402B-8	Sequence 8, Appli
21	477	85.6	106	1	US-08-326-362-4	Sequence 4, Appli
22	438	78.6	106	1	US-08-436-463-20	Sequence 20, Appl
23	438	78.6	108	2	US-09-232-290-27	Sequence 27, Appl
24	438	78.6	109	1	US-06-107-669D-1	Sequence 1, Appli
25	435	78.1	107	1	US-07-942-245-4	Sequence 4, Appli
26	435	78.1	107	1	US-08-472-788A-1	Sequence 1, Appli
27	435	78.1	107	1	US-08-477-531B-1	Sequence 1, Appli
28	435	78.1	107	1	US-08-082-842A-1	Sequence 1, Appli
29	425	76.3	107	1	US-07-634-278-62	Sequence 62, Appl
30	425	76.3	107	1	US-08-474-040-62	Sequence 62, Appl
31	425	76.3	107	1	US-08-487-200-62	Sequence 62, Appl
32	425	76.3	107	2	US-08-484-537-62	Sequence 62, Appl
33	425	76.3	107	1	US-07-634-278-83	Sequence 83, Appl
34	425	76.3	107	1	US-08-474-040-83	Sequence 83, Appl
35	425	76.3	107	1	US-08-487-200-83	Sequence 83, Appl
36	425	76.3	127	1	US-08-484-537-83	Sequence 83, Appl
37	425	75.8	127	1	US-08-436-463-4	Sequence 4, Appli
38	422	75.8	127	1	US-08-485-246A-6	Sequence 6, Appli
39	417	74.9	127	1	US-08-476-176B-6	Sequence 6, Appli
40	417	74.9	127	1	US-08-127-721A-6	Sequence 6, Appli
41	417	74.9	127	2	US-08-485-246A-6	Sequence 6, Appli
42	417	74.9	127	2	US-08-436-463-18	Sequence 18, Appl
43	415	74.5	127	1	US-08-476-176B-8	Sequence 8, Appli
44	413	74.1	127	1	US-08-476-176B-8	Sequence 8, Appli
45	413	74.1	127	2	US-08-127-721A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-476-176B-4
Sequence 4, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; APPLICATION DATA:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-176B-4

Query Match 89.4%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
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Db 1 DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTDGSPRLLIKYASESISGIPS 60

Qy 61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
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      ||||||||| : :|| |||||||||||||||||: || |||||||||
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Db 61 RFSGSGSGTEFTLNINSVESEDIADYYCQQSDSWPTTFGGGTKLEIK 107

RESULT 2
US-08-127-721A-4
; Sequence 4, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-127-721A-4

Query Match 89.4%; Score 498; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
Db 1 DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTDGSPRLLIKYASESISGIPS 60

Qy 61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
Db 61 RFSGSGSGTEFTLNINSVESEDIADYYCQQSDSWPTTFGGGTKLEIK 107

RESULT 3
US-08-485-246A-4
; Sequence 4, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,246A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6072035ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-246A-4

Query Match 89.4%; Score 498; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 2.8e-39;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPPRLLIKNVSESISGIPS 60
Db 1 DILLTQSPAILSVSPGERVSFSCRASQSIGTNIHWYQQRTDGSPRLLIKYASESISGIPS 60

Qy 61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
Db 61 RFSGSGSGTEFTLNINSVESEDIADYYCQQSDSWPTTFGGGTKLEIK 107

RESULT 4
US-09-244-369B-1
; Sequence 1, Application US/09244369B
; Patent No. 6418838
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; TITLE OF INVENTION: Method for detecting and surgically removing lymphoid tissue invol
; FILE REFERENCE: Phy-01
; CURRENT APPLICATION NUMBER: US/09/244,369B
; CURRENT FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 60/073,882
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: US 60/077,970
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 17:22:45 ; Search time 137.504 Seconds
(without alignments)
549.012 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILLTQSPAILSVSPGERVS..........CQQSNTWPFTFGGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Pred. No	Query Match Length	DB	ID	Description
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2	395	70.9	262	2	Q65ZI1_MOUSE	Q65zi1	mus musculu
3	358.5	64.4	235	2	Q6GMW0_HUMAN	Q6gmw0	homo sapien
4	357	64.1	108	2	Q9UL83_HUMAN	Q9ul83	homo sapien
5	354.5	63.6	108	2	Q9UL85_HUMAN	Q9ul85	homo sapien
6	353	63.4	108	2	Q8VIJ0_MOUSE	Q8vij0	mus musculu
7	350.5	62.9	109	1	KV3F_HUMAN	P01624	homo sapien
8	348.5	62.6	114	2	Q8K1F1_MOUSE	Q8k1f1	mus musculu
9	348	62.5	128	1	KV3K_HUMAN	P06311	homo sapien
10	347.5	62.4	129	1	KV3H_HUMAN	P04207	homo sapien
11	343	61.6	111	1	KV3H_MOUSE	P01660	mus musculu
12	339	60.9	111	1	Q5F2I7_MOUSE	Q5f2i7	mus musculu
13	338	60.7	111	2	Q92OB9_MOUSE	Q92ob9	mus musculu
14	338	60.7	238	2	Q66JS7_MOUSE	Q66js7	mus musculu
15	335	60.1	111	1	KV3L_MOUSE	P01664	mus musculu
16	333	59.8	236	2	Q6GMX9_HUMAN	Q6gmx9	homo sapien
17	332.5	59.7	108	1	Q9UL78_HUMAN	Q9ul78	homo sapien
18	332	59.6	108	1	KV1M_HUMAN	P01605	homo sapien
19	332	59.6	111	1	KV3M_MOUSE	P01665	mus musculu
20	332	59.6	111	1	KV3R_MOUSE	P01670	mus musculu
21	331.5	59.5	112	2	Q8K1F3_MOUSE	Q8k1f3	mus musculu
22	329.5	59.2	111	2	Q65ZN3_MOUSE	Q65zn3	mus musculu
23	329	59.1	111	1	KV3O_MOUSE	P01667	mus musculu
24	328.5	59.0	235	2	Q6GMV9_HUMAN	Q6gmv9	homo sapien
25	327.5	58.8	237	2	Q56Y8_MOUSE	Q56y8	mus musculu
26	327	58.7	129	1	KV3S_MOUSE	P01671	mus musculu
27	326.5	58.6	129	1	KV3L_HUMAN	P18135	homo sapien
28	326	58.5	108	1	KV5K_MOUSE	P01644	mus musculu
29	326	58.5	108	1	KV5O_MOUSE	P01648	mus musculu
30	326	58.5	234	2	Q4KM66_RAT	Q4km66	rattus norv
31	326	58.5	236	2	Q6PIH7_HUMAN	Q6pih7	homo sapien
32	325	58.3	236	2	Q6GMX8_HUMAN	Q6gmx8	homo sapien
33	324.5	58.3	134	2	Q8VDD0_MOUSE	Q8vdd0	mus musculu
34	324	58.2	108	1	KV5L_MOUSE	P01645	mus musculu
35	324	58.2	108	1	KV5N_MOUSE	P01647	mus musculu
36	324	58.2	108	2	Q9UL79_HUMAN	Q9ul79	homo sapien
37	324	58.2	111	2	KV3N_MOUSE	P01666	mus musculu
38	324	58.2	136	1	KV3U_MOUSE	P01673	mus musculu
39	323	58.0	111	1	KV5B_MOUSE	P01634	mus musculu
40	323	58.0	108	1	KV1Y_HUMAN	P80362	homo sapien
41	323	58.0	108	1	KV3Q_MOUSE	P01669	mus musculu
42	323	58.0	111	2	Q81IU6_MOUSE	Q81iu6	mus musculu
43	322.5	57.9	234	2	Q7Z473_HUMAN	Q7z473	homo sapien
44	322.5	57.9	107	2	Q96SA9_HUMAN	Q96sa9	homo sapien
45	322.5	57.9	108	2	KV3A_HUMAN	P01619	homo sapien

ALIGNMENTS

RESULT 1
KV5I_MOUSE

ID   KV5I_MOUSE   STANDARD;   PRT;   115 AA.
AC   P01642;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update).
DE   Ig kappa chain V-V region L7 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
CC   -!- MISCELLANEOUS: There appears to be two possible splice junctions
CC   at the 3' end of the intron. The alternate would code for a
CC   protein lacking residues 17-19.
CC   -!-
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -!-
DR   PIR; A01925; KVMSL7.
DR   PDB; 1C08; X-ray; A=22-115.
DR   PDB; 1IC4; X-ray; L=22-115.
DR   PDB; 1IC5; X-ray; L=22-115.
DR   PDB; 1IC7; X-ray; L=22-115.
DR   PDB; 1J1O; X-ray; L=22-115.
DR   PDB; 1J1P; X-ray; L=22-115.
DR   PDB; 1J1X; X-ray; L=22-114.
DR   Ensembl; ENSMUSG00000029975; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   >115   Ig kappa chain V-V region L7.
FT   REGION   21   43   Framework-1.
FT   REGION   44   54   Complementarity-determining-1.
FT   REGION   55   69   Framework-2.
FT   REGION   70   76   Complementarity-determining-2.
FT   REGION   77   108   Framework-3.
FT   REGION   109   >115   Complementarity-determining-3.
FT   DISULFID   43   108   By similarity.
FT   NON_TER   115   115

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FT   STRAND       24     27
FT   STRAND       30     33
FT   TURN         35     36
FT   TURN         39     45
FT   STRAND       50     51
FT   STRAND       53     58
FT   TURN         60     61
FT   STRAND       65     69
FT   STRAND       65     72
FT   TURN         70     72
FT   TURN         73     74
FT   STRAND       76     77
FT   TURN         80     81
FT   TURN         82     87
FT   STRAND       88     89
FT   TURN         90     95
FT   HELIX       100    102
FT   STRAND      104    110
SQ   SEQUENCE    115 AA;  12615 MW;  C17BEC758C577E00 CRC64;

Qy   Query Match           81.7%;  Score 455;  DB 1;  Length 115;
     Best Local Similarity   92.6%;  Pred. No. 2.9e-40;
     Matches    88;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS  60
         |:||||||||||||||||||||||:|||||||:||||||||||::||::|||||||||||
Db   21  DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASESISGIPS  80

Qy   61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWP  95
         |||||||||||:|||||||||||||||||||||:||
Db   81  RFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWP  115
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RESULT 2
Q65ZI1   MOUSE

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ID   Q65ZI1_MOUSE  PRELIMINARY;     PRT;   262 AA.
AC   Q65ZI1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Anti-HIV-1 reverse transcriptase single-chain variable.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Hybridoma;
RX   MEDLINE=96211469; PubMed=8648670;
RA   Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT   "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT   by intracellular expression of single-chain variable fragments to
RT   inhibit early stages of the viral life cycle.";
RL   J. Virol. 70:3392-3400(1996).
DR   EMBL; U48716; AAB64342.1; -; mRNA.
DR   SMR; Q65ZI1; 2-132.
DR   GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; RNA-directed DNA polymerase.
SQ   SEQUENCE   262 AA;  27842 MW;  7DF20138E53865E4 CRC64;

Qy   Query Match           70.9%;  Score 395;  DB 2;  Length 262;
     Best Local Similarity   69.2%;  Pred. No. 1.9e-33;
     Matches    74;  Conservative    15;  Mismatches    18;  Indels    0;  Gaps    0;

Qy    1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS  60
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Db    2  DIIMTQSPAILSVTPGDRVSLSCRASQSISDFLHWYQQKSHESPRLLIKYASQSISGIPS  61

Qy   61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107
         |||||||||:|||||||:||||::|||:|||||| |||||||:|||:|
Db   62  RFSGSGSGSDFTLSINSVEPEDVGVYYCQNGHSFPLITFGAGTKLELK  108
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RESULT 3
Q6GMW0   HUMAN

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ID   Q6GMW0_HUMAN  PRELIMINARY;     PRT;   235 AA.
AC   Q6GMW0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKV1-5 protein.
GN   Name=IGKV1-5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   Director MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073792; AAH73792.1; -; mRNA.
DR   SMR; Q6GMW0; 21-233.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

Qy   Query Match           64.4%;  Score 358.5;  DB 2;  Length 235;
     Best Local Similarity   64.8%;  Pred. No. 1.2e-29;
     Matches    70;  Conservative    13;  Mismatches    24;  Indels    1;  Gaps    1;

Qy    1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS  60
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OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: February 15, 2006, 17:32:01 ; Search time 22.9956 Seconds
(without alignments)
447.702 Million cell updates/sec

Title: US-10-524-134-4
Perfect score: 557
Sequence: 1 DILITQSPAILSVSPGERVS..........CQQSNTWPFTFGGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	503	90.3	108	2	C30502	Ig kappa chain V r
2	499	89.6	128	2	PN0445	Ig kappa chain pre
3	455	81.7	115	1	KVMSL7	Ig kappa chain pre
4	425	76.3	107	2	A45722	Ig kappa chain pre
5	424	76.1	107	2	B45722	anti-glycoprotein
6	423	75.9	123	2	S35479	anti-glycoprotein
7	421	75.6	106	2	PL0267	Ig kappa chain pre
8	418	75.0	102	2	S26346	Ig kappa chain V r
9	415	74.5	107	2	C45722	anti-glycoprotein
10	415	74.5	138	2	A26471	anti-glycoprotein
11	408.5	73.3	87	2	PH1082	Ig kappa chain pre
12	408	73.2	104	2	B43413	Ig kappa chain V r
13	384	68.9	103	2	S19975	Ig kappa chain V r
14	377.5	67.8	215	2	JE0244	Ig kappa chain NIG
15	376	67.5	117	2	S40362	Ig kappa chain - h
16	370	66.4	144	2	PL0106	Ig kappa chain pre
17	365	65.5	128	2	S40343	Ig kappa chain V-J
18	360	64.6	111	2	S23628	Ig kappa chain V r
19	359	64.5	107	2	S34005	Ig kappa chain V r
20	357.5	64.2	114	2	S54905	Ig kappa chain NIG
21	356	63.9	215	2	JE0243	Ig kappa chain NIG
22	354	63.6	108	2	S19674	Ig kappa chain V r
23	352	63.2	106	2	PC4282	Ig kappa chain (an
24	352	63.2	128	2	A44151	Ig kappa chain V r
25	352	63.2	128	2	A56701	Ig kappa chain V r
26	350.5	62.9	109	1	K3HUPM	Ig kappa chain V-I
27	349	62.7	125	2	S40344	Ig kappa chain V-J
28	348	62.5	128	1	K3HU41	Ig kappa chain pre
29	348	62.5	129	2	S29627	Ig lambda chain V
30	347	62.3	128	2	S40379	Ig kappa chain V-J
31	345	61.9	107	2	A28195	Ig kappa chain V r
32	343	61.6	111	1	KVMS37	Ig kappa chain V r
33	342.5	61.5	109	2	G30607	Ig kappa chain V-I
34	342.5	61.5	131	2	B02636	Ig kappa chain - h
35	342	61.4	128	2	S40328	Ig kappa chain V-J
36	341.5	61.3	116	2	B26555	anti-DNA autoantib
37	341	61.2	108	2	PL0204	Ig kappa chain V-J
38	341	61.2	125	2	PL0204	Ig kappa chain V-J
39	340.5	61.1	120	2	S09963	Ig light chain V r
40	340.5	61.1	111	2	S66536	Ig kappa chain V-J
41	340	61.0	117	2	B49047	Ig kappa chain V r
42	339	60.9	108	2	S42466	Ig kappa chain V r
43	339	60.9	129	2	S40317	Ig kappa chain V-J
44	339	60.9	132	2	S40334	Ig kappa chain - h
45	338	60.7	107	2	S36269	Ig lambda chain v

ALIGNMENTS

RESULT 1
C30502
Ig kappa chain V region (D444) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
A;Accession: C30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <BIL>
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Cross-references: UNIPARC:UPI000011ADCF; GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   90.3%; Score 503; DB 2; Length 108;
Best Local Similarity   89.7%; Pred. No. 1.3e-38;
Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy   1 DILITQSPAILSVSPGERVSFSCRTSQSISGTNIHWYQQRTNGFPRLLIKNVSESISGIPS 60
             ||||||||||||||||||||||||:||||||::||||||||||||||||||||||||||||
Db   1 DILITQSPAILSVSPGERVSFSCRASQSIGTSLHWYQQRTNGSPRLLIKYASESISGIPS 60

Qy   61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
             |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107

RESULT 2
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0445
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymeras
A;Reference number: PN0444; MUID:93138402; PMID:1333379
A;Accession: PN0445
A;Molecule type: mRNA
A;Residues: 1-128 <KAL>
A;Cross-references: UNIPARC:UPI00001767795; GB:L02347
A;Species: UNIPARC:UPI000017C795; GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   89.6%;   Score 499;   DB 2;   Length 128;
                        89.7%;   Pred. No. 3.5e-38;
Matches 96;   Conservative   5;   Mismatches   6;   Indels   0;   Gaps   0;

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Qy   1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  11 DVILTQSPAILSVSPGERVSFSCRASQSISIHWYQRYGNGPPRLLIKYASESISGIPS 70

Qy  61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
        ||||||||||||||||:|||||||||||||||||||||||
Db  71 RFSGSGSGTDFTLSISSVESEDIADYYCQQTNSWPTIFGGGTKLEIK 117
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RESULT 3
KVMSL7
Ig kappa chain precursor V region (L7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C;Accession: A01925
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequ
A;Reference number: A93259; MUID:81220975; PMID:6264318
A;Accession: A01925
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: UNIPROT:P01642; UNIPARC:UPI000023365; GB:V01564; GB:J00574; NID:g951
A;Note: the sequence was determined from the germline gene
A;Note: there appear to be two possible splice junctions at the 3' end of the intron; th
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
F;43-108/Disulfide bonds: #status predicted

Query Match
Best Local Similarity   81.7%;   Score 455;   DB 1;   Length 115;
                        92.6%;   Pred. No. 2.9e-34;
Matches 88;   Conservative   2;   Mismatches   5;   Indels   0;   Gaps   0;

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Qy   1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
        |||||||||||||||||||||:|||||||||||||||||||||||||||
Db  21 DILLTQSPAILSVSPGERVSFSCRASQSISIHWYQQRTNGSPRLLIKYASESISGIPS 80

Qy  61 RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWP 95
        |||||||||||||||||||||||||||||:||
Db  81 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWP 115
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RESULT 4
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A;Reference number: A45722; MUID:9310833; PMID:7677958
A;Molecule type: mRNA
A;Residues: 1-107 <SIM>
A;Cross-references: UNIPARC:UPI00000144CFD
A;Note: sequence extracted from NCBI backbone (NCBIP:120589)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   76.3%;   Score 425;   DB 2;   Length 107;
                        73.8%;   Pred. No. 1.4e-31;
Matches 79;   Conservative 12;   Mismatches 16;   Indels   0;   Gaps   0;

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Qy   1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
        |:||||||||||||||||::||||:||||||||:|:||||||||||||:||||||||
Db   1 DIVLTQSPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHSSPRLLIKYASQSISGIPS 60

Qy  61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
        ||||||||||||||||||||||||||||||:||||||||||||
Db  61 RFSGSGSGTDFTLSVNGVETEDFGMYFCQQTNSWPHTFGGGTKLEIK 107
```

RESULT 5
B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hun
A;Reference number: A45722; MUID:9310833; PMID:7677958
A;Accession: B45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-107 <SIM>
A;Cross-references: UNIPARC:UPI00001767AF
A;Note: sequence extracted from NCBI backbone (NCBIP:120590)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   76.1%;   Score 424;   DB 2;   Length 107;
                        73.8%;   Pred. No. 1.7e-31;
Matches 79;   Conservative 13;   Mismatches 15;   Indels   0;   Gaps   0;

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Qy   1 DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGPPRLLIKNVSESISGIPS 60
        |:||||||||:|||||:||||||:||||||||:|:|||||||||||||:||||||||
Db   1 DIVLTQSPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHSSPRLLIKYASQSISGIPS 60

Qy  61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK 107
        |||||||||||||||:|:||||||||||||:||||||||||||
Db  61 RFSGSGSGTDFTLSVNGVETEDFGMYFCQQTNSWPHTFGGGTKLEIK 107
```

RESULT 6
S35479
Ig kappa chain precursor V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S35479
A;Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a mo
R;Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A;Map position: 6
A;Genetics:
C;Accession: S35479
A;Cross-references: UNIPARC:UPI000115359; EMBL:M93959; NID:g1975572; PIDN:AAA39079.1; PII
A;Molecule type: DNA
A;Residues: 1-123 <TAK>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F;13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F;28-102/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity   75.9%;   Score 423;   DB 2;   Length 123;
                        74.8%;   Pred. No. 2.4e-31;
Matches 80;   Conservative 12;   Mismatches 15;   Indels   0;   Gaps   0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:　　　　February 15, 2006, 17:22:00 ; Search time 262.338 Seconds
　　　　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　　　　　　179.210 Million cell updates/sec

Title:　　　　US-10-524-134-4
Perfect score:　557
Sequence:　　1 DILLTQSPAILSVSPGERVS..........CQQSNTWPFTFGGGTKLEIK 107
Scoring table:　BLOSUM62
Searched:　　Gapop 10.0 , Gapext 0.5
　　　　　　　　2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:　　2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

Database :　A_Geneseq_21:*
　　　　　1: geneseqp1980s:*
　　　　　2: geneseqp1990s:*
　　　　　3: geneseqp2000s:*
　　　　　4: geneseqp2001s:*
　　　　　5: geneseqp2002s:*
　　　　　6: geneseqp2003aa:*
　　　　　7: geneseqp2003bs:*
　　　　　8: geneseqp2004s:*
　　　　　9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	557	100.0	107	8	ADL00215	Human Fcg
2	510	91.6	214	8	AEC20776	M-CSF spe
3	504	90.5	107	9	ADY31675	Anti-IL9
4	504	90.5	108	7	ADG75665	Humanised
5	504	90.5	109	8	ABB99223	Chimeric
6	504	90.5	214	9	AEC20766	M-CSF spe
7	503	90.3	214	9	AEC20765	M-CSF spe
8	503	90.3	107	3	AAB10023	H. pylori
9	503	90.3	107	4	AAB86109	H. pylori
10	503	90.3	107	4	AAB86071	H. pylori
11	503	90.3	107	5	ABB99221	Part of c
12	503	90.3	124	9	ADY80249	Fragment
13	503	90.3	107	9	AEC07204	Murine NY
14	503	90.3	107	5	AEC07178	NYR-1002
15	503	90.3	214	9	ABB99223	Chimeric
16	500	89.8	214	9	ADY80251	Amino aci
17	500	89.8	107	2	AAU72860	Human p53
18	499	89.6	107	5	AAU72850	Human
19	499	89.6	107	9	AAR32129	Anti-NKG2
20	499	89.6	107	9	ADJ80369	Antibody
21	499	89.6	107	7	AEA48149	Mouse ant
22	499	89.6	127	2	AEB13698	Human ant
23	499	89.6	127	2	AAW08945	Kappa lig
24	499	89.6	127	2	AAW08943	Kappa lig
25	499	89.6	234	8	ADS14301	EGFR ligh
26	499	89.6	236	8	ADP44635	Murine an
27	499	89.6	236	9	AEA60461	Mouse ant
28	498	89.4	107	2	AAR50190	Light cha
29	498	89.4	107	2	AAY26979	Light cha
30	498	89.4	107	8	ADR43401	Murine an
31	498	89.4	107	8	ADR31546	Murine TE
32	498	89.4	107	8	ADR87520	Mouse ant
33	498	89.4	107	8	AEC08122	Murine mA
34	498	89.4	107	8	AAB31426	Protein u
35	498	89.4	242	4	AAY31610	Mucin Tn
36	498	89.4	244	4	AAB31425	Protein u
37	497	89.2	244	4	AAU72842	Anti-NKG2
38	497	89.2	510	5	AAU72859	65SA7x4-7
39	496	89.0	107	7	ADJ80370	FR homolo
40	495	88.9	651	2	AAW05135	scFv(225)
41	495	88.9	892	2	AAW05140	scFv2(225
42	495	88.9	892	2	AAW05139	scFv2(FRP
43	495	88.9	1020	2	AAW05141	scFv2(FRP
44	494	88.9	127	2	AAW44176	Monoclona
45	493	88.5	106	9	AEA40019	Mouse ant

ALIGNMENTS

RESULT 1
ID　ADL00215
AC　ADL00215;
XX
DT　20-MAY-2004　(first entry)
XX
DE　Human FcgammaRIIB antibody light chain.
XX
KW　cytostatic; antirheumatic; antiarthritic; antipsoriatic; dermatological;
KW　immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW　immunosuppressive; nephrotropic; ophthalmological;
KW　B cell receptor-mediated signaling modulator;
KW　Fc gamma RI-induced mast cell activation modulator;
KW　B cell activation modulator; B cell proliferation modulator;
KW　antibody production modulator; intracellular calcium influx modulator;
KW　vaccine composition efficacy enhancer; gene therapy; FcgammaRIIB; cancer;
KW　breast cancer; ovarian cancer; prostate cancer; cervical cancer;
KW　pancreatic cancer; chemotherapy; immunotherapy; radiation therapy;
KW　hormonal therapy; autoimmune disorder; rheumatoid arthritis;
KW　psoriatic arthritis; ankylosing spondylitis; Rieter's Syndrome;
KW　psoriasis; lupus erythematosus; IgE-mediated allergic disorder; asthma;
KW　allergic rhinitis; gastrointestinal allergy; eosinophilia;
KW　conjunctivitis; glomerular nephritis; autoimmune disease; vaccine;
KW　B cell malignancy; non-Hodgkin's lymphoma; solid tumour;
KW　fragment of crystallisation gamma receptor IIB; antibody light chain;
KW　human.
XX
OS　Homo sapiens.
XX
PN　WO200401675O-A2.
XX
PD　26-FEB-2004.
XX
PF　14-AUG-2003; 2003WO-US025399.
PR　14-AUG-2002; 2002US-0403266P.
XX
PA　(MACR-) MACROGENICS INC.
XX
PI　Koenig S,　Veri M;
XX
DR　WPI; 2004-203783/19.
DR　N-PSDB; ADL00214.
XX
PT　Novel isolated antibody or its fragment useful for treating diseases

```
PT   e.g., cancer, that specifically binds native FcgammaRIIB with greater
PT   affinity than antibody or its fragment that binds native FcgammaRIIA.
XX
PS   Disclosure; SEQ ID NO 4; 174pp; English.
XX
CC   The invention describes an isolated antibody or its fragment (I) that
CC   specifically binds native FcgammaRIIB. (I) is useful for treating cancer
CC   (e.g., breast, ovarian, prostate, cervical or pancreatic cancer) in a
CC   patient (e.g., human) having cancer with specific cancer antigen which
CC   involves administering a first antibody or its fragment which is (I) and
CC   a second antibody that specifically binds the cancer antigen and is
CC   cytotoxic. The above method further involves administration of one or
CC   more additional cancer therapies such as chemotherapy, immunotherapy,
CC   radiation therapy, hormonal therapy, or surgery. (I) is useful for
CC   treating an autoimmune disorder e.g. rheumatoid arthritis, psoriatic
CC   arthritis, ankylosing spondylitis, Rieter's Syndrome, psoriasis, or lupus
CC   erythematosus. The above method further involves administering to the
CC   patient a therapeutically effective amount of one or more anti-
CC   inflammatory agents or immunomodulatory agents e.g., small organic
CC   molecule such as methotrexate or corticosteroid. The anti-inflammatory
CC   agent is a non-steroidal anti-inflammatory drug e.g. aspirin or
CC   ketoprofen. (I) is also useful for: treating IgE-mediated allergic
CC   disorder such as asthma, allergic rhinitis, gastrointestinal allergies,
CC   eosinophilia, conjunctivitis, or glomerular nephritis; enhancing an
CC   antibody mediated cytotoxic effect in a subject; diagnosing an autoimmune
CC   disease in a subject; enhancing an immune response to a vaccine
CC   composition in a subject; treating a B cell malignancy (e.g., non-
CC   Hodgkin's lymphoma; treating a disease in a patient; treating a solid
CC   tumour in a patient; and treating cancer in a patient. (I) has an altered
CC   affinity for an FcgammaR. (I) antibody binds FcgammaRIIB with a higher
CC   affinity than a comparable antibody comprising a wild-type Fc region
CC   binds FcgammaRIIB. (I) has an enhanced antibody mediated effector
CC   function relative to a comparable antibody comprising a wild-type Fc
CC   region. This is the amino acid sequence of human fragment of
CC   crystallisation gamma receptor IIB (FcgammaRIIB) antibody light chain.
XX
SQ   Sequence 107 AA;

Query Match             100.0%;  Score 557;  DB 8;  Length 107;
Best Local Similarity   100.0%;  Pred. No. 6.7e-41;
Matches  107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPRLLIKNVSESISGIPS  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPRLLIKNVSESISGIPS  60

Qy         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107


RESULT 2
ID   AEC20776 standard; protein; 214 AA.
XX
AC   AEC20776;
XX
DT   20-OCT-2005  (first entry)
XX
DE   M-CSF specific murine antibody MC-3 light chain SEQ ID NO 15.
XX
KW   endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
KW   antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;
KW   cardiovascular-gen.; degeneration; eating-disorders-gen.;
KW   endocrine disease; endocrine-gen.; gastrointestinal-gen.;
KW   genetic disorder; light chain; hepatotropic; hypercalcemia;
KW   immune disorder; immunotherapy; inflammation; monoclonal antibody;
KW   mouth disease; musculoskeletal disease; neoplasm; nephrotropic;
KW   osteopathic; osteoporosis; osteopetrosis; Pages disease;
KW   periodontal disease; pharmaceutical; rheumatoid arthritis; MC-3.
XX
OS   Mus musculus.
XX
PN   WO200506503-A2.
XX
PD   28-JUL-2005.
XX
PF   06-JAN-2005; 2005WO-US000546.
XX
PR   07-JAN-2004; 2004US-0533181P.
PR   02-JUN-2004; 2004US-0576417P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (XOMA ) XOMA TECHNOLOGY LTD.
XX
PI   Liu C, Zimmerman DL, Harrowe GM, Kotha K, Kavanaugh WM, Long L;
PI   Calderon-Cacia M, Horwitz AH;
XX
DR   WPI; 2005-597707/61.
XX
PT   Novel non-murine antibody that competes with monoclonal antibody RX1 for
PT   binding to macrophage colony stimulating factor, useful for treating
PT   hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
PT   osteoporosis.
XX
PS   Example 10; SEQ ID NO 15; 269pp; English.
XX
CC   The invention describes a non-murine antibody (I) that competes with
CC   monoclonal antibody RX1 for binding to macrophage colony stimulating
CC   factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has
CC   the heavy chain and light chain amino acid sequences having a fully
CC   defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)
CC   sequences given in the specification, respectively. (I) is useful for
CC   preventing a subject afflicted with a disease that causes or contributes
CC   to osteolysis, where the antibody effectively reduces the severity of
CC   bone loss associated with the disease. The disease is chosen from
CC   metabolic bone diseases associated with relatively increased osteoclast
CC   activity, including endocrinopathies, hypercalcemia, deficiency states,
CC   chronic diseases, and hereditary diseases; cancer, osteoporosis,
CC   osteopetrosis, inflammation of bone associated with arthritis and/or
CC   rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or
CC   Paget's disease. (I) is useful for preventing or treating metastatic
CC   cancer. Antibodies of the invention are useful for preventing or reducing
CC   bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is
CC   useful for manufacturing a medicament for preventing or reducing bone
CC   loss in a patient exhibiting osteolysis, manufacturing a medicament for
CC   treating a patient afflicted with a disease that causes or contributes to
CC   osteolysis, and metastatic cancer to bone in a patient suffering from
CC   metastatic cancer, for manufacturing a medicament for treating a patient
CC   having cancer. (I) in synergistic combination, is useful for Preparing a
CC   medicament for treating a patient exhibiting osteolysis. This is the
CC   amino acid sequence of macrophage colony stimulating factor (M-CSF)
CC   specific murine antibody MC-3 light chain.
XX
SQ   Sequence 214 AA;

Query Match             91.6%;   Score 510;  DB 9;  Length 214;
Best Local Similarity   92.5%;   Pred. No. 1.7e-36;
Matches  99;  Conservative  2;  Mismatches  6;  Indels  0;  Gaps  0;

Qy          1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPRLLIKNVSESISGIPS  60
               |||||||||||||||||||||||| ||||||| |||||||||| |||||| ||||||||||
Db          1  DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASESISGIPS  60

Qy         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107
               ||||||||||||||||||||||||||||||||| || ||||||||||
Db         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNSWPTFGGGTKLEIK  107


RESULT 3
ID   ADY31675 standard; protein; 107 AA.
XX
AC   ADY31675;
XX
DT   05-MAY-2005  (first entry)

Query Match             100.0%;  Score 557;  DB 8;  Length 107;
Best Local Similarity   100.0%;  Pred. No. 6.7e-41;
Matches  107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPRLLIKNVSESISGIPS  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1  DILLTQSPAILSVSPGERVSFSCRTSQSIGTNIHWYQQRTNGFPRLLIKNVSESISGIPS  60

Qy         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         61  RFSGSGSGTDFILSINSVESEDIADYYCQQSNTWPFTFGGGTKLEIK  107
```

OM protein - protein search, using sw model

```
                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.
```

Run on: February 15, 2006, 17:53:06 ; Search time 11.6754 Seconds
                                     (without alignments)
                                     147.285 Million cell updates/sec

Title: US-10-524-134-2
Perfect score: 651
Sequence: 1 QVQLQQPVTELVRPGASVML.........SDYSGMDYWGQGTSVTVSS 121

Scoring table: BLOSUM62
Sequence: Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Published Applications AA New:*
              1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
              2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
              3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
              4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
              5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
              6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
              7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
              8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

•   Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	651	100.0	121	7	US-11-108-135-28	Sequence 28, Appl
2	651	100.0	121	7	US-11-126-978-28	Sequence 28, Appl
3	529	81.3	121	7	US-11-126-978-24	Sequence 24, Appl
4	529	81.3	121	7	US-11-126-978-24	Sequence 24, Appl
5	502.5	77.2	122	7	US-10-932-334-73	Sequence 73, Appl
6	460.5	70.7	118	7	US-11-126-798-48	Sequence 48, Appl
7	457.5	70.3	120	7	US-10-932-334-72	Sequence 72, Appl
8	453	69.6	113	7	US-11-177-648-7	Sequence 7, Appli
9	453	69.6	462	7	US-11-177-648-9	Sequence 9, Appl
10	452.5	69.5	120	7	US-10-932-334-71	Sequence 71, Appl
11	452.5	69.5	248	6	US-10-512-184-36	Sequence 36, Appl
12	452.5	69.5	615	6	US-10-512-184-50	Sequence 50, Appl
13	450.5	69.2	120	6	US-10-982-357-3	Sequence 3, Appli
14	450	69.1	119	7	US-11-221-900-10	Sequence 10, Appl
15	449	69.0	117	6	US-10-932-334-76	Sequence 76, Appl
16	448.5	68.9	120	6	US-10-932-334-74	Sequence 74, Appl
17	448.5	68.9	120	6	US-10-932-334-78	Sequence 78, Appl
18	445.5	68.4	124	6	US-10-932-334-7	Sequence 7, Appli
19	445.5	68.4	124	6	US-10-932-334-13	Sequence 13, Appl
20	445.5	68.4	124	6	US-10-932-334-70	Sequence 70, Appl
21	445.5	68.4	143	6	US-10-932-334-52	Sequence 52, Appl
22	444	68.2	666	7	US-11-096-046-29	Sequence 29, Appl
23	444	68.2	667	7	US-11-981-356A-29	Sequence 29, Appl
24	441.5	67.8	116	7	US-11-055-163-17	Sequence 17, Appl
25	441.5	67.8	123	6	US-10-932-334-87	Sequence 87, Appl
26	441.5	67.8	123	6	US-10-932-334-88	Sequence 88, Appl
27	441.5	67.8	123	6	US-10-932-334-92	Sequence 92, Appl
28	441	67.7	121	6	US-10-507-662-26	Sequence 26, Appl
29	436	67.0	121	6	US-10-507-662-25	Sequence 25, Appl
30	435	66.8	116	7	US-11-507-812-19	Sequence 19, Appl
31	435	66.8	121	7	US-11-107-028-35	Sequence 35, Appli
32	432.5	66.4	129	7	US-11-179-820-4	Sequence 4, Appli
33	432	66.4	121	6	US-10-932-334-81	Sequence 81, Appl
34	430.5	66.1	120	6	US-10-932-334-75	Sequence 75, Appl
35	429.5	66.0	118	6	US-10-665-658-4	Sequence 4, Appli
36	429	66.0	121	6	US-10-932-334-75	Sequence 75, Appl
37	429	65.9	121	7	US-11-107-028-52	Sequence 52, Appli
38	429	65.9	133	7	US-11-149-031-4	Sequence 4, Appli
39	429	65.9	247	7	US-11-084-717-21	Sequence 21, Appli
40	428	65.7	247	7	US-11-069-834-2	Sequence 2, Appli
41	428	65.7	247	7	US-11-084-717-21	Sequence 21, Appli
42	428	65.7	247	7	US-11-179-244-21	Sequence 21, Appli
43	427.5	65.7	111	7	US-11-084-055B-21	Sequence 21, App
44	427.5	65.7	111	6	US-11-097-812-205	Sequence 205, Appl
45	423	65.0	113	7	US-11-177-648-15	Sequence 15, Appl
```

ALIGNMENTS

RESULT 1
US-11-108-135-28
Sequence 28, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuaillon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse 2B6 heavy chain variable region
US-11-108-135-28

  Query Match   100.0%; Score 651; DB 7; Length 121;
  Best Local Similarity   100.0%;
  Matches 121; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60

Qy   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120

Qy   121 S 121
               |
Db   121 S 121

RESULT 2
US-11-126-978-28
Sequence 28, Application US/11126978
Publication No. US20060013810A1
GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie Sydnor
; APPLICANT: Huang, Ling
; TITLE OF INVENTION: HUMANIZED FcgammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THER
; FILE REFERENCE: 11183-018-999
; CURRENT APPLICATION NUMBER: US/11/126,978
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 60/582,043
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/569,882
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse 2B6 heavy chain variable region

Query Match   100.0%; Score 651; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.2e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60

Qy   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120

Qy 121 S 121
          |
Db 121 S 121

RESULT 3
US-11-108-135-24
Sequence 24, Application US/11108135
Publication No. US20050260213A1
GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuaillon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence

; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-108-135-24

Query Match   95; Score 529; DB 7; Length 121;
Best Local Similarity 78.5%; Pred. No. 2.3e-37;
Matches 95; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
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Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIHWVRQAPGQGLEWIGVIDPSDTYPNY 60

Qy   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
          ||||||:.|:|:| :|:|:|:| ||||:|||||||||||||||||||||||||:||||
Db   61 NKKFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARNGDSDYYSGMDYWGQGTTVTVS 120

Qy 121 S 121
          |
Db 121 S 121

RESULT 4
US-11-126-978-24
Sequence 24, Application US/11126978
Publication No. US20060013810A1
GENERAL INFORMATION:
; APPLICANT: Johnson, Leslie Sydnor
; APPLICANT: Huang, Ling
; TITLE OF INVENTION: HUMANIZED FcgammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THERE
; FILE REFERENCE: 11183-018-999
; CURRENT APPLICATION NUMBER: US/11/126,978
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 60/582,043
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/569,882
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain variable region
US-11-126-978-24

Query Match   81.3%; Score 529; DB 7; Length 121;
Best Local Similarity 78.5%; Pred. No. 2.3e-37;
Matches 95; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
          |||| || | :|| ||| ||||| :|||||||||||:: ||||||:||||||||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIHWVRQAPGQGLEWMGVIDPSDTYPNY 60

Qy   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
          ||||||:.|:|:| :|:|:|:| ||||:|||||||||||||||||||||||||:||||
Db   61 NKKFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARNGDSDYYSGMDYWGQGTTVTVS 120

Qy 121 S 121
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Db 121 S 121

RESULT 5
US-10-932-334-73
Sequence 73, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A6689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: February 15, 2006, 17:52:22 ; Search time 119.939 seconds
(without alignments)
421.527 Million cell updates/sec

Title: US-10-524-134-2
Perfect score: 651
Sequence: 1 QVQLQQPVTELVRPGASVML.........SDYYSGMDYWGQGTSVTVSS 121
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	651	100.0	121	5	4	US-10-643-857-2	Sequence 2, Appli
2	651	100.0	121	5	4	US-10-524-134-2	Sequence 2, Appli
3	502.5	77.2	122	5	US-10-729-441-73	Sequence 73, Appl
4	502.5	77.2	122	5	US-10-897-406-73	Sequence 73, Appl
5	492.5	75.7	242	4	US-10-259-087A-18	Sequence 18, Appl
6	492.5	75.7	242	4	US-10-689-006-18	Sequence 18, Appl
7	491.5	75.5	118	5	US-10-816-938-23	Sequence 23, Appl
8	489	75.1	140	3	US-09-748-960-4	Sequence 9, Appli
9	487	74.8	464	4	US-10-216-484-9	Sequence 9, Appli
10	487	74.8	464	4	US-10-384-933-9	Sequence 9, Appli
11	483.5	74.3	120	4	US-10-096-246-12	Sequence 12, Appl
12	472	72.5	143	4	US-10-010-729-66	Sequence 66, Appl
13	469	72.0	365	5	US-10-880-028-44	Sequence 44, Appl
14	469	72.0	365	5	US-10-880-320-44	Sequence 44, Appl
15	467.5	71.8	118	4	US-10-435-614-20	Sequence 20, Appl
16	467.5	71.8	260	4	US-10-435-614-11	Sequence 11, Appl
17	467.5	71.8	467	4	US-10-742-405-12	Sequence 12, Appl
18	464.5	71.4	122	2	US-08-779-784-28	Sequence 28, Appl
19	462.5	71.0	122	5	US-10-895-135-63	Sequence 63, Appl
20	461	70.8	143	2	US-08-779-784-26	Sequence 26, Appl
21	458.5	70.4	118	4	US-10-436-782-5	Sequence 5, Appli
22	458.5	70.4	118	4	US-10-436-795A-5	Sequence 5, Appli
23	458.5	70.4	118	6	US-11-004-794A-5	Sequence 5, Appli
24	458.5	70.4	121	5	US-10-879-994-82	Sequence 82, Appl
25	458.5	70.4	248	5	US-10-879-994-14	Sequence 14, Appl
26	458.5	70.4	248	5	US-10-610-552-14	Sequence 14, Appl
27	457.5	70.3	118	4	US-10-435-614-13	Sequence 13, Appl
28	457.5	70.3	120	4	US-10-351-748-24	Sequence 24, Appl
29	457.5	70.3	120	4	US-10-351-748-24	Sequence 24, Appl
30	457.5	70.3	120	4	US-10-729-441-72	Sequence 72, Appl
31	457.5	70.3	122	5	US-10-897-406-72	Sequence 72, Appl
32	457.5	70.3	122	4	US-10-096-246-10	Sequence 10, Appl
33	457.5	70.3	177	4	US-10-435-614-21	Sequence 21, Appl
34	457.5	70.3	122	4	US-10-435-614-21	Sequence 21, Appl
35	455	69.9	138	4	US-10-163-942-78	Sequence 78, Appl
36	455	69.9	138	5	US-10-753-436-78	Sequence 78, Appl
37	455	69.9	138	4	US-09-753-436-78	Sequence 78, Appl
38	452.5	69.5	118	5	US-10-789-090-9	Sequence 9, Appli
39	452.5	69.5	120	5	US-10-729-441-71	Sequence 71, Appl
40	452.5	69.5	120	5	US-10-895-135-57	Sequence 57, Appl
41	452.5	69.4	120	5	US-10-897-406-71	Sequence 71, Appl
42	451.5	69.2	126	4	US-10-312-316-44	Sequence 44, Appl
43	450.5	69.2	120	5	US-10-312-316-44	Sequence 44, Appl
44	450	69.1	116	3	US-09-940-727B-17	Sequence 17, Appl
45	450	69.1	119	3	US-09-795-515-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-643-857-2

Sequence 2, Application US/10643857

; Publication No. US20040185045A1
; GENERAL INFORMATION:
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Koenig, Scott
; TITLE OF INVENTION: Anti-FcgRIIB monoclonal antibodies and their use in enhancing
; FILE REFERENCE: 11183-010-999
; CURRENT APPLICATION NUMBER: US/10/643,857
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,266
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-643-857-2

Query Match   100.0%; Score 651; DB 4; Length 121;
Best Local Similarity   100.0%; Pred. No. 9e-52;
Matches 121; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
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Db   1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60

Qy   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120

Qy 121 S 121
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Db 121 S 121

RESULT 2
US-10-524-134-2

Sequence 2, Application US/10524134

; Publication No. US20050215767A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; TITLE OF INVENTION: Anti-FcgRIIB monoclonal antibodies and their use in enhancing
; TITLE OF INVENTION: immune response
; FILE REFERENCE: 11183-003-999
; CURRENT APPLICATION NUMBER: US/10/524,134

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;    CURRENT FILING DATE: 2005-02-11
;    PRIOR APPLICATION NUMBER: PCT/US03/25399
;    PRIOR FILING DATE: 2003-08-14
;    PRIOR APPLICATION NUMBER: 60/403,266
;    PRIOR FILING DATE: 2002-08-14
;    NUMBER OF SEQ ID NOS: 4
;    SOFTWARE: PatentIn version 3.2
;
;    SEQ ID NO 2
;    LENGTH: 121
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-524-134-2

Query Match             100.0%;  Score 651;  DB 5;  Length 121;
Best Local Similarity   100.0%;  Pred. No. 9e-52;
Matches 121;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60
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Db    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS  120
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Db   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS  120

Qy  121  S  121
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Db  121  S  121


RESULT 3
US-10-729-441-73
;    Sequence 73, Application US/10729441
;    Publication No. US20040265307A1
;    GENERAL INFORMATION:
;    APPLICANT: ImmunoGen, Inc.
;    TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
;    FILE REFERENCE: A8689
;    CURRENT APPLICATION NUMBER: US/10/729,441
;    CURRENT FILING DATE: 2003-12-08
;    PRIOR APPLICATION NUMBER: 10/170,390
;    PRIOR FILING DATE: 2002-06-14
;    NUMBER OF SEQ ID NOS: 96
;    SOFTWARE: PatentIn version 3.2
;
;    SEQ ID NO 73
;    LENGTH: 122
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic antibody structure
US-10-729-441-73

Query Match             77.2%;  Score 502.5;  DB 5;  Length 122;
Best Local Similarity   78.6%;  Pred. No. 3.3e-38;
Matches 99;  Conservative 7;  Mismatches 11;  Indels 9;  Gaps 2;

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Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQGPGQGLEWIGEIDPSDSYPNY  60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSG-----MDYWGQGT  115
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Qy  116  SVTVSS  121
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Db  117  SVTVSS  122


RESULT 4
US-10-897-406-73
;    Sequence 73, Application US/10897406
;    Publication No. US2005018203A1
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;    GENERAL INFORMATION:
;    APPLICANT: ImmunoGen, Inc.
;    TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
;    FILE REFERENCE: A8338
;    CURRENT APPLICATION NUMBER: US/10/897,406
;    CURRENT FILING DATE: 2004-07-23
;    PRIOR APPLICATION NUMBER: US/10/170,390
;    PRIOR FILING DATE: 2002-06-14
;    NUMBER OF SEQ ID NOS: 96
;    SOFTWARE: PatentIn version 3.1
;
;    SEQ ID NO 73
;    LENGTH: 122
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic antibody structure
US-10-897-406-73

Query Match             77.2%;  Score 502.5;  DB 5;  Length 122;
Best Local Similarity   78.6%;  Pred. No. 3.3e-38;
Matches 99;  Conservative 7;  Mismatches 11;  Indels 9;  Gaps 2;

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Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSG-----MDYWGQGT  115
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Qy  116  SVTVSS  121
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Db  117  SVTVSS  122


RESULT 5
US-10-259-087A-18
;    Sequence 18, Application US/10259087A1
;    Publication No. US20030130190A1
;    GENERAL INFORMATION:
;    APPLICANT: Vanderbilt University
;    APPLICANT: Hallahan, Dennis E
;    APPLICANT: Qu, Shimian
;    TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
;    FILE REFERENCE: 1242/47/2
;    CURRENT APPLICATION NUMBER: US/10/259,087A
;    CURRENT FILING DATE: 2002-09-27
;    PRIOR APPLICATION NUMBER: US 60/328123
;    PRIOR FILING DATE: 2001-10-03
;    NUMBER OF SEQ ID NOS: 20
;    SOFTWARE: PatentIn version 3.1
;
;    SEQ ID NO 18
;    LENGTH: 242
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Artificial antibody ligand number 1
US-10-259-087A-18

Query Match             75.7%;  Score 492.5;  DB 4;  Length 242;
Best Local Similarity   77.7%;  Pred. No. 5.7e-37;
Matches 94;  Conservative 9;  Mismatches 15;  Indels 3;  Gaps 1;

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Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS  120
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Qy  121  S  121
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Db  121  S  121
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OM protein - protein search, using sw model

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GenCore version 5.1.7

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285.607 Million cell updates/sec

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Perfect score: 651
Sequence: 1 QVQLQQPVTELVRPGASVML........SDYYSGMDYWGQGTSVTVSS 121

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Maximum DB seq length: 200000000
Minimum DB seq length: 0

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	Match	DB	ID	Description
1	493	75.7	119	1		US-08-553-497A-12	Sequence 12, Appl
2	483.5	74.3	120	2		US-10-092-246-12	Sequence 12, Appl
3	483.5	74.3	120	2		US-10-096-246A-12	Sequence 12, Appl
4	481	73.9	119	2		US-08-553-497A-8	Sequence 8, Appli
5	477	73.3	119	2		US-08-881-037-62	Sequence 62, Appl
6	477	73.3	445	1		US-08-353-400-33	Sequence 33, Appl
7	477	73.3	464	1		US-08-353-400-36	Sequence 36, Appl
8	475	73.0	119	2		US-08-881-037-60	Sequence 60, Appl
9	475	73.0	119	2		US-08-881-037-61	Sequence 61, Appl
10	474	72.8	119	2		US-09-423-439-38	Sequence 38, Appl
11	474	72.8	288	2		US-09-423-439-32	Sequence 32, Appl
12	473	72.7	673	2		US-08-881-037-63	Sequence 63, Appl
13	471	72.4	119	2		US-09-406-532-2	Sequence 2, Appli
14	466	71.6	119	2		US-09-254-180C-16	Sequence 16, Appl
15	466	71.6	119	2		US-09-254-180C-149	Sequence 149, App
16	466	71.6	138	2		US-09-913-555-23	Sequence 23, Appl
17	466	71.6	219	2		US-09-254-180C-143	Sequence 143, Appl
18	466	71.6	219	2		US-09-254-180C-180	Sequence 180, App
19	464.5	71.4	122	4		US-08-236-520-9	Sequence 9, Appli
20	464.5	71.4	122	4		PCT-US95-05262-9	Sequence 9, Appl
21	463	71.1	111	2		US-08-881-037-14	Sequence 14, Appl
22	463	71.1	111	2		US-09-065-059-5	Sequence 5, Appli
23	463	71.1	118	2		US-08-913-555-5	Sequence 5, Appli
24	461	70.8	111	2		US-08-881-037-15	Sequence 15, Appl
25	461	70.8	111	2		US-08-236-520-7	Sequence 7, Appli
26	461	70.8	143	4		PCT-US95-05262-7	Sequence 7, Appli
27	460.5	70.7	118	2		US-08-766-350B-48	Sequence 48, Appl
28	460.5	70.7	269	1		US-08-428-257A-72	Sequence 72, Appl
29	460.5	70.7	269	1		US-08-491-988-3	Sequence 3, Appli
30	460.5	70.7	402	1		US-08-491-988-9	Sequence 9, Appli
31	460.5	70.7	415	1		US-08-491-988-7	Sequence 7, Appli
32	460.5	70.7	435	1		US-08-491-988-5	Sequence 5, Appli
33	460	70.7	111	2		US-08-881-037-16	Sequence 16, Appl
34	459	70.5	111	2		US-10-092-246-10	Sequence 10, Appl
35	457.5	70.3	122	2		US-10-092-246-11	Sequence 11, Appl
36	457.5	70.3	122	2		US-10-096-246A-11	Sequence 11, Appl
37	457.5	70.3	122	2		US-10-096-246A-10	Sequence 10, Appl
38	457.5	70.3	241	2		US-08-465-473B-11	Sequence 11, Appl
39	456.5	70.1	241	2		US-08-235-838-11	Sequence 11, Appl
40	456.5	70.1	637	1		US-08-465-473B-16	Sequence 16, Appl
41	456.5	70.1	637	1		US-08-235-838-16	Sequence 16, Appl
42	456.5	70.1	139	1		US-08-894-922A-5	Sequence 5, Appli
43	456	70.0	139	1		US-08-894-922A-14	Sequence 14, Appl
44	456	70.0	252	1		US-08-894-922A-10	Sequence 10, Appl
45	456	70.0	271	1		US-08-894-922A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-553-497A-12

; Sequence 12, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAIR, JAUME
; APPLICANT: MITJANS, FRANSESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 12:

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;   SEQUENCE CHARACTERISTICS:
;      LENGTH: 119 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;   US-08-553-497A-12

Qy    Query Match            75.7%;  Score 493; DB 1; Length 119;
Db    Best Local Similarity  79.5%;  Pred. No. 7.6e-37;
      Matches 97; Conservative 8; Mismatches 13; Indels 4; Gaps 2;

Qy    1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVUIDPSDTYPNY 60
        ||||||:|||||||||||||||||:||||:||||||||||||||||||||||:|||
Db    1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTNY 60

Qy   61 NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSG-MDYWGQGTSVTV 119
        ||||||||||:|||||||||||||||||:|||||:||| |:|||||:|||
Db   61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR---SDYGSSHFDYWGQGTTVTV 117

Qy  120 SS 121
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Db  118 SS 119
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RESULT 2
US-10-092-246-12
;   Sequence 12, Application US/10092246
;   Patent No. 6501314
;   GENERAL INFORMATION:
;      APPLICANT: The Minister of National Defence, Government of Canada
;      APPLICANT: Nagata, Leslie
;      APPLICANT: Alvi, Azhar E
;      APPLICANT: Fulton, R E
;      TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;      FILE REFERENCE: NEL-0007
;      CURRENT APPLICATION NUMBER: US/10/092,246
;      CURRENT FILING DATE: 2002-03-13
;      NUMBER OF SEQ ID NOS: 37
;      SOFTWARE: Patentin version 3.1
;      SEQ ID NO 12
;      LENGTH: 120
;      TYPE: PRT
;      ORGANISM: Mouse hybridoma cell line 1A4A1
;   US-10-092-246-12

Qy    Query Match            74.3%;  Score 483.5; DB 2; Length 120;
Db    Best Local Similarity  76.6%;  Pred. No. 5.4e-36;
      Matches 95; Conservative 7; Mismatches 15; Indels 7; Gaps 2;

Qy    1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVUIDPSDTYPNY 60
        ||||||:|||||||||||||||||:||||:||||||||||||||||||||||:||
Db    1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTY 60

Qy   61 NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYS---GMDYWGQGTSV 117
        ||||||||||:|||||||||||||||||:||||||:||       |:||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQFSSLTSEDSAVYYCARR----YYGSRVSMDYWGQGTSV 116

Qy  118 TVSS 121
        ||||
Db  117 TVSS 120
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RESULT 3
US-10-096-246A-12
;   Sequence 12, Application US/10096246A
;   Patent No. 6818748
;   GENERAL INFORMATION:
;      APPLICANT: Fulton, R. Elaine
;      APPLICANT: Nagata, Leslie
;      APPLICANT: Alvi, Azhar Z.
;      TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
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;      TITLE OF INVENTION: Virus (VEE)
;      FILE REFERENCE: NEL-0007
;      CURRENT APPLICATION NUMBER: US/10/096,246A
;      CURRENT FILING DATE: 2002-03-13
;      NUMBER OF SEQ ID NOS: 39
;      SOFTWARE: Patentin version 3.2
;   US-10-096-246A-12
;      SEQ ID NO 12
;      LENGTH: 120
;      TYPE: PRT
;      ORGANISM: mouse
;   US-10-096-246A-12

Qy    Query Match            74.3%;  Score 483.5; DB 2; Length 120;
Db    Best Local Similarity  76.6%;  Pred. No. 5.4e-36;
      Matches 95; Conservative 7; Mismatches 15; Indels 7; Gaps 2;

Qy    1 QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVUIDPSDTYPNY 60
        ||||||:|||||||||||||||||:||||:||||||||||||||||||||||:||
Db    1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTY 60

Qy   61 NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYS---GMDYWGQGTSV 117
        ||||||||||:|||||||||||||||||:||||||:||       |:||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQFSSLTSEDSAVYYCARR----YYGSRVSMDYWGQGTSV 116

Qy  118 TVSS 121
        ||||
Db  117 TVSS 120
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```
RESULT 4
US-08-553-497A-8
;   Sequence 8, Application US/08553497A
;   Patent No. 5844093
;   GENERAL INFORMATION:
;      APPLICANT: KETTLEBOROUGH, C. A.
;      APPLICANT: BENDIG, MARY M.
;      APPLICANT: ANSELL, KEITH H.
;      APPLICANT: GUSSOW, DETLEF
;      APPLICANT: ADAN, JAUME
;      APPLICANT: MITJANS, FRANSESC
;      APPLICANT: ROSELL, ELISABET
;      APPLICANT: BLASCO, FRANCESC
;      APPLICANT: PIULATS, JAUME
;      TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;      TITLE OF INVENTION: ANTIBODIES
;      NUMBER OF SEQUENCES: 30
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET: 2200 CLARENDON BLVD. SUITE 1400
;      CITY: ARLINGTON
;      STATE: VA
;      COUNTRY: US
;      ZIP: 22201
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/553,497A
;      FILING DATE: 17-NOV-1995
;      CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/EP95/00978
;      FILING DATE: 16-MAR-1995
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: EP 94104160.0
;      FILING DATE: 17-MAR-1994
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: EP 94118970.6
;      FILING DATE: 02-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;      NAME: HAMLET-KING, DIANA
```

```
                                        GenCore version 5.1.7
                         Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:           February 15, 2006, 17:22:45 ; Search time 155.496 Seconds
                                                 (without alignments)
                                                 549.012 Million cell updates/sec

Title:            US-10-524-134-2
Perfect score:    651
Sequence:         1 QVQLQQPVTELVRPGASVML...........SDYSGMDYWGQGTSVTVSS 121

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:  2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
             1:   uniprot_sprot:*
             2:   uniprot_trembl:*

'   Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	495	76.0	142	2	Q92AQ2_MOUSE	Q92aq2 mus musculu
2	491.5	75.5	143	2	Q91V67_MOUSE	Q91v67 mus musculu
3	487	74.8	142	2	Q91WT3_MOUSE	Q91wt3 mus musculu
4	483	74.2	616	2	Q9JL81_MOUSE	Q9jl81 mus musculu
5	481.5	74.0	482	2	Q924P9_MOUSE	Q924p9 mus musculu
6	475	73.0	482	2	Q8K172_MOUSE	Q8k172 mus musculu
7	474.5	72.9	145	2	Q924P7_MOUSE	Q924p7 mus musculu
8	474.5	72.9	145	2	Q924P6_MOUSE	Q924p6 mus musculu
9	474.5	72.9	145	2	Q924R4_MOUSE	Q924r4 mus musculu
10	472.5	72.6	145	2	Q924R1_MOUSE	Q924r1 mus musculu
11	470.5	72.3	143	2	Q924Q9_MOUSE	Q924q9 mus musculu
12	467	71.8	143	2	Q924R0_MOUSE	Q924r0 mus musculu
13	462	71.0	140	2	Q924P8_MOUSE	Q924p8 mus musculu
14	460	70.7	146	2	Q924Q3_MOUSE	Q924q3 mus musculu
15	460	70.7	146	2	Q924R8_MOUSE	Q924r8 mus musculu
16	457.5	70.3	139	1	HV07_MOUSE	P01751 mus musculu
17	457.5	70.3	140	2	Q924Q7_MOUSE	Q924q7 mus musculu
18	457	70.2	140	2	Q924R2_MOUSE	Q924r2 mus musculu
19	454.5	69.8	617	2	Q4KML5_MOUSE	Q4kml5 mus musculu
20	452	69.4	138	1	HV48_MOUSE	P03980 mus musculu
21	448.5	68.9	143	2	Q924Q5_MOUSE	Q924q5 mus musculu
22	448.5	68.9	488	2	Q8K0F2_MOUSE	Q8k0f2 mus musculu
23	447.5	68.7	144	2	Q924P5_MOUSE	Q924p5 mus musculu
24	447	68.7	144	2	Q924P6_MOUSE	Q924p6 mus musculu
25	446.5	68.6	141	2	Q924Q4_MOUSE	Q924q4 mus musculu
26	445.5	68.4	137	2	Q924R6_MOUSE	Q924r6 mus musculu
27	444	68.2	146	2	Q924Q8_MOUSE	Q924q8 mus musculu
28	443.5	68.1	143	2	Q924R7_MOUSE	Q924r7 mus musculu
29	441.5	67.8	143	2	Q924Q0_MOUSE	Q924q0 mus musculu
30	441.5	67.8	145	2	Q924R3_MOUSE	Q924r3 mus musculu
31	441.5	67.8	590	2	Q4V9V8_MOUSE	Q4v9v8 mus musculu
32	439.5	67.5	136	2	Q7TPE3_MOUSE	Q7tpe3 mus musculu
33	438.5	67.4	143	2	Q91VA2_MOUSE	Q91va2 mus musculu
34	437	67.1	481	2	Q91WT3_MOUSE	Q91wt3 mus musculu
35	435.5	66.9	114	2	Q9JL81_MOUSE	Q9jl81 mus musculu
36	434	66.7	140	1	HV02_MOUSE	P01746 mus musculu
37	434	66.7	468	2	Q569W9_MOUSE	Q569w9 mus musculu
38	431.5	66.3	486	2	Q5HZY6_MOUSE	Q5hzy6 mus musculu
39	430	66.1	458	2	Q924R5_MOUSE	Q924r5 mus musculu
40	428.5	65.8	139	2	Q5BJZ2_RAT	Q5bjz2 rattus norv
41	428	65.7	120	2	Q9D8L4_MOUSE	Q9d8l4 mus musculu
42	427.5	65.3	120	1	HV50_MOUSE	P06329 mus musculu
43	425	65.3	473	1	HV03_MOUSE	P01747 mus musculu
44	421.5	64.7	110	2	Q9JL77_MOUSE	Q9jl77 mus musculu
45	421	64.7	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculu

ALIGNMENTS

RESULT 1
Q92AQ2_MOUSE

```
ID   Q92AQ2_MOUSE PRELIMINARY;          PRT;   142 AA.
AC   Q92AQ2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   V303-D-J-C mu protein (Fragment).
GN   Name=V303-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069910; BAB63926.1; -; mRNA.
DR   HSSP; P01751; 1A6W.
DR   Ensembl; ENSMUSG00000061773; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     142    142
SQ   SEQUENCE   142 AA;  15684 MW;  048809F90C0FBD7B CRC64;

Query Match             76.0%;  Score 495;  DB 2;  Length 142;
Best Local Similarity   78.5%;  Pred. No. 1.7e-41;
Matches   95;  Conservative    7;  Mismatches  15;  Indels   4;  Gaps   1;

Qy    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60
            |||||| :|||||||||||||:|:|: |||||||||||||||||||:|||||| :|
Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGPEWIGEIDPSDIYTDY  60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYISGMDYWGQGTSVTVS 120
            |::|:||||||| ||:|||||||||:|||||||||||              :|||||||
Db   61  NQEFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYYCARR-----YGGQDYWGQGTSVTVS 116
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RESULT 2
Q91V67_MOUSE

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ID   Q91V67_MOUSE PRELIMINARY;          PRT;   143 AA.
AC   Q91V67;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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DE   VH186.D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN   Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RX   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069912; BAB63928.1; -; mRNA.
DR   EMBL; AB069913; BAB63930.1; -; mRNA.
DR   PIR; S26744; S26744.
DR   HSSP; Q91V67; 1A6W.
DR   SMR; Q91V67; 1-129.
DR   InterPro; IPR007110; Ig-like.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   143   143
SQ   SEQUENCE   143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match   75.5%; Score 491.5; DB 2; Length 143;
Best Local Similarity   78.5%; Pred. No. 3.8e-41;
Matches   95; Conservative   7; Mismatches 16; Indels   3; Gaps   1;

Qy   1 QVQLQQPGTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
              | |||||| ||||||||| |||||||||||||||||||||||||||||| |||||||||
Db   1 QVQLQQPGAELVRPGTSVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGVIDPSDSYTNY 60

Qy   61 NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
              || |||||||| ||||||||||||||||| |||||||| ||| |||||||||||
Db   61 NQKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYYCAPTVDDWYF---DVWGTGTTVTVS 117

Qy   121 S 121
              |
Db   118 S 118

RESULT 3
ID   Q92401 MOUSE PRELIMINARY;   PRT;   142 AA.
AC   Q92401;
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   V23-D-J-C mu protein (Fragment).
GN   Name=AB069917; Synonyms=V23-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RX   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN   [3]
RX   Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;

RT   "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT   C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT   specific V genes as the original antigen.";
RL   J. Immunol. 141:779-784(1988).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA   Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT   "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT   selective B cell stimulation in (NZB x NZW)F1 mice.";
RL   J. Exp. Med. 176:761-779(1992).
DR   EMBL; AB069913; BAB63929.1; -; mRNA.
DR   PIR; F33932; F33932.
DR   PIR; I28833; I28833.
DR   PIR; PH0985; PH0985.
DR   PIR; PH1155; PH1155.
DR   PIR; PH1156; PH1156.
DR   PIR; PH1157; PH1157.
DR   PIR; PH1158; PH1158.
DR   HSSP; P01751; 1A6W.
DR   SMR; Q92401; 1-128.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   MGI; MGI:3576502; AB069917.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   142   142
SQ   SEQUENCE   142 AA; 15622 MW; 24A265CE4BA4318B CRC64;

Query Match   74.8%; Score 487; DB 2; Length 142;
Best Local Similarity   78.5%; Pred. No. 1.1e-40;
Matches   95; Conservative   8; Mismatches 14; Indels   4; Gaps   1;

Qy   1 QVQLQQPGTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY 60
              | |||||| ||||||||| ||||||||||| |||||||||||||||||||||||| |||
Db   1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNY 60

Qy   61 NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
              || |||||||| ||||||||||||||||| |||||||| |||||||||||||||
Db   61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRG---WEAMDYWGQGTSVTVS 116

Qy   121 S 121
              |
Db   117 S 117

RESULT 4
ID   Q504M7 MOUSE PRELIMINARY;   PRT;   616 AA.
AC   Q504M7;
DT   13-SEP-2005 (TREMBLrel. 31, Created)
DT   13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22382557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

OM protein - protein search, using sw model

Run on: February 15, 2006, 17:22:00 ; Search time 296.662 seconds
(without alignments)
179.210 Million cell updates/sec

Title: US-10-524-134-2
Perfect score: 651
Sequence: 1 QVQLQQPVTELVRPGASVML.........SDYYSGMDYWGQGTSVTVSS 121
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues
                2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_21:*
            1: geneseqp1980s:*
            2: geneseqp1990s:*
            3: geneseqp2000s:*
            4: geneseqp2010s:*
            5: geneseqp2020s:*
            6: geneseqp2003ab:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
            9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	651	100.0	121	8	ADL00213	Adl00213 Human Fcg
2	502.5	77.2	122	8	ADH17833	Adh17833 Murine an
3	502.5	77.2	122	9	ADW11464	Adw11464 Murine an
4	502	77.1	119	8	ADP79380	Adp79380 Thyrotrop
5	502	77.1	124	8	ADP79384	Adp79384 Thyrotrop
6	493	75.7	119	2	AAR79863	Aar79863 Anti-EGFR
7	492.5	75.7	242	8	ABR62131	Abr62131 Single ch
8	492.5	75.7	242	8	ADT91207	Adt91207 Single ch
9	491.5	75.5	118	8	ADU39962	Adu39962 Antibody
10	491	75.4	118	2	AAW07436	Aaw07436 Anti-DNA
11	489	75.1	140	2	AAW53815	Aaw53815 Murine Ac
12	489	75.1	140	5	AAU11177	Aau11177 Mouse ant
13	489	75.1	144	2	AAW53816	Aaw53816 Consensus
14	487	74.8	464	2	AAW83041	Aaw83041 Anti-Fas
15	487	74.8	464	3	AAB14747	Aab14747 Mouse ant
16	487	74.8	464	2	AAW90897	Aaw90897 Murine an
17	487	74.8	464	5	ABB74912	Abb74912 Humanised
18	487	74.8	464	5	ABB74866	Abb74866 Humanised
19	482	74.0	466	9	ADX39137	Adx39137 Mouse mon
20	482	74.0	466	9	ADX39100	Adx39100 Mouse mon
21	481	73.9	119	2	AAR79861	Aar79861 Anti-EGFR
22	477	73.3	137	2	AAW53818	Aaw53818 Protein s
23	477	73.3	445	2	AAR76085	Aar76085 MAb 55.1
24	477	73.3	464	2	AAR76088	Aar76088 MAb 55.1
25	474.5	72.9	123	9	Adz45377	Adz45377 Murine fa
26	474	72.8	288	2	Aaw82743	Aaw82743 Fusion pr
27	474	72.8	673	2	Aaw82742	Aaw82742 Plasmid p
28	472	72.5	117	8	Adf77173	Adf77173 Anti-VAP-
29	472	72.5	119	8	Adg25806	Adg25806 Anti-CD30
30	472	72.5	119	8	Adg25812	Adg25812 Anti-CD30
31	471.5	72.4	143	8	Adi26636	Adi26636 Human ant
32	471	72.4	123	8	Adz45369	Adz45369 Murine fa
33	469	72.1	365	9	Aay92156	Aay92156 Murine 15
34	469	72.1	123	3	Adw77071	Adw77071 Heavy cha
35	468.5	72.0	123	9	Adz45373	Adz45373 Murine fa
36	468.5	72.0	118	9	Adz45365	Adz45365 Murine fa
37	467.5	71.8	260	9	Adz21533	Adz21533 Anti-Muc-
38	467.5	71.8	122	9	Adz21542	Adz21542 Anti-Muc-
39	466.5	71.7	467	8	Adq14477	Adq14477 Mouse ant
40	466	71.6	119	2	Aaw00835	Aaw00835 Variable
41	466	71.6	138	2	Adz45353	Adz45353 Murine fa
42	464.5	71.4	121	9	Aaw50218	Aaw50218 Amino aci
43	464.5	71.4	122	2	Adz45353	Adz45353 Murine fa
44	464.5	71.4	309	4	Aar84555	Aar84555 B-cell ly
45	463	71.1	111	2	Aab70841	Aab70841 SNV-env 1
					Aaw04586	Aaw04586 Anti-DNA

ALIGNMENTS

RESULT 1
ADL00213

ID   ADL00213 standard; protein; 121 AA.
AC   ADL00213;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Human FcgammaRIIB antibody heavy chain.
XX
KW   cytostatic; antirheumatic; antiarthritic; antipsoriatic; dermatological;
KW   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW   immunosuppressive; nephrotropic; ophthalmological;
KW   B cell receptor-mediated signaling modulator;
KW   Fc gamma RI-induced mast cell activation modulator;
KW   B cell activation modulator; B cell proliferation modulator;
KW   antibody production modulator; intracellular calcium influx modulator;
KW   vaccine composition efficacy enhancer; gene therapy; FcgammaRIIB; cancer;
KW   breast cancer; ovarian cancer; prostate cancer; cervical cancer;
KW   pancreatic cancer; chemotherapy; immunotherapy; radiation therapy;
KW   hormonal therapy; autoimmune disorder; rheumatoid arthritis;
KW   psoriatic arthritis; ankylosing spondylitis; Rieter's Syndrome;
KW   psoriasis; lupus erythematosus; IgE-mediated allergic disorder; asthma;
KW   allergic rhinitis; gastrointestinal allergy; eosinophilia;
KW   conjunctivitis; glomerular nephritis; autoimmune disease; vaccine;
KW   B cell malignancy; non-Hodgkin's lymphoma; solid tumour;
KW   fragment of crystallisation gamma receptor IIB; antibody heavy chain;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO2004016750-A2.
PD   26-FEB-2004.
PF   14-AUG-2003; 2003WO-US025399.
PR   14-AUG-2002; 2002US-0403266P.
XX
PA   (MACR-) MACROGENICS INC.
PI   Koenig S, Veri M;
XX
PT   Novel isolated antibody or its fragment useful for treating diseases
XX
DR   WPI; 2004-203783/19.
DR   N-PSDB; ADL00212.
XX

```
PT   e.g., cancer, that specifically binds native FcgammaRIIB with greater
PT   affinity than antibody or its fragment that binds native FcgammaRIIA.
XX
PS   Disclosure; SEQ ID NO 2; 174pp; English.
XX
CC   The invention describes an isolated antibody or its fragment (I) that
CC   specifically binds native FcgammaRIIB. (I) is useful for treating cancer
CC   (e.g., breast, ovarian, prostate, cervical or pancreatic cancer) in a
CC   patient (e.g., human) having cancer with specific cancer antigen which
CC   involves administering a first antibody or its fragment which is (I) and
CC   a second antibody that specifically binds the cancer antigen and is
CC   cytotoxic. The above method further involves administration of one or
CC   more additional cancer therapies such as chemotherapy, immunotherapy,
CC   radiation therapy, hormonal therapy, or surgery. (I) is useful for
CC   treating an autoimmune disorder e.g. rheumatoid arthritis, psoriatic
CC   arthritis, ankylosing spondylitis, Rieter's Syndrome, Psoriasis, or lupus
CC   erythematosus. The above method further involves administering to the
CC   patient a therapeutically effective amount of one or more anti-
CC   inflammatory agents or immunomodulatory agents e.g., small organic
CC   molecule such as methotrexate or corticosteroid. The anti-inflammatory
CC   agent is a non-steroidal anti-inflammatory drug e.g. aspirin or
CC   ketoprofen. (I) is also useful for: treating IgE-mediated allergic
CC   disorder such as asthma, allergic rhinitis, gastrointestinal allergies,
CC   eosinophilia, conjunctivitis, or glomerular nephritis; enhancing an
CC   antibody mediated cytotoxic effect in a subject; diagnosing an autoimmune
CC   disease in a subject; enhancing an immune response to a vaccine
CC   composition in a subject; treating a B cell malignancy (e.g., non-
CC   Hodgkin's lymphoma; treating a disease in a patient; treating a solid
CC   tumour in a patient; and treating cancer in a patient. (I) has an altered
CC   affinity for an FcgammaR. (I) antibody binds FcgammaRIIB with a higher
CC   affinity than a comparable antibody comprising a wild-type Fc region
CC   binds FcgammaRIIIA. (I) has an enhanced antibody mediated effector
CC   function relative to a comparable antibody comprising a wild-type Fc
CC   region. This is the amino acid sequence of human fragment of
CC   crystallisation gamma receptor IIB (FcgammaRIIB) antibody heavy chain.
XX
SQ   Sequence 121 AA;

Query Match             100.0%;  Score 651;  DB 8;  Length 121;
Best Local Similarity   100.0%;  Pred. No. 5.2e-47;
Matches 121;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60

Qy   61  NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSGMDYWGQGTSVTVS 120

Qy  121  S 121
         |
Db  121  S 121
```

```
RESULT 2
ID   ADH17833 standard; protein; 122 AA.
XX
AC   ADH17833;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Murine antibody 1fbi heavy chain variable region protein.
XX
KW   antibody EM164; insulin-like growth factor-I receptor; IGF-IR antagonist;
KW   breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
KW   prostate; lung; synovial carcinoma; pancreatic; murine; mouse;
KW   heavy chain variable region; 1fbi.
XX
OS   Mus sp.
XX
PN   WO200310621-A2.
XX
PD   24-DEC-2003.
XX
PF   12-JUN-2003; 2003WO-US016211.
XX
PR   14-JUN-2002; 2002US-00170390.
XX
PA   (IMMU-) IMMUNOGEN INC.
XX
PI   Singh R, Tavares DJ, Dagdigian NE;
XX
DR   WPI; 2004-082172/08.
XX
PT   Novel murine antibody EM164 or antibody fragment that specifically binds
PT   to insulin-like growth factor-I-receptor useful for treating breast
PT   cancer, colon cancer, lung cancer, prostate cancer.
XX
PS   Example 2; SEQ ID NO 73; 155pp; English.
XX
CC   The invention relates to a novel murine antibody EM164 or antibody
CC   fragment that specifically binds to insulin-like growth factor-I receptor
CC   (IGF-IR) where the antibody is an antagonist of the receptor, is
CC   substantially devoid of agonist activity toward the receptor and is
CC   capable of inhibiting the growth of a cancer cell by greater than 80% in
CC   the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
CC   The antibody of the invention may be useful for diagnosing or treating
CC   patient having a cancer selected from breast cancer, colon cancer,
CC   ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
CC   cancer, synovial carcinoma and pancreatic cancer. The current sequence is
CC   that of the murine anti-IGF-IR antibody EM164-related protein of the
CC   invention.
XX
SQ   Sequence 122 AA;

Query Match             77.2%;  Score 502.5;  DB 8;  Length 122;
Best Local Similarity   78.6%;  Pred. No. 1.5e-34;
Matches  99;  Conservative  7;  Mismatches 11;  Indels  9;  Gaps  2;

Qy    1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY  60
         :.|||||| ||||:|||||:|||||| ||| :.||:||||| |||||||||||||:.|||
Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQGPGQGLEWIGEIDPSDSYPNY  60

Qy   61  NKKFKGKATLTVVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSG-----MDYWGQGT 115
         |:||||||||||  .|||||||||||||:||||||||          :.||  |||||||
Db   61  NEKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA----SLYYYGTSYGVLDYWGQGT 116

Qy  116  SVTVSS 121
         ||||||
Db  117  SVTVSS 122
```

```
RESULT 3
ID   ADW11464 standard; protein; 122 AA.
XX
AC   ADW11464;
XX
DT   24-MAR-2005  (first entry)
XX
DE   Murine anti-IGF 1 receptor antibody EM164 VH-homologous 1fbi protein.
XX
KW   antibody; cytostatic; cancer; neoplasm; breast tumor; colon tumor;
KW   uterine cervix tumor; prostatic cancer; lung tumor; pancreas tumor;
KW   ovary tumor; carcinoma; osteosarcoma; melanoma; nervous system tumor;
KW   gene therapy; heavy chain variable region.
XX
OS   Unidentified.
XX
PN   US2004265307-A1.
XX
PD   30-DEC-2004.
XX
PF   08-DEC-2003; 2003US-00729441.
```

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: February 15, 2006, 17:32:01 ; Search time 26.0044 Seconds
(without alignments)
447.702 Million cell updates/sec

Title: US-10-524-134-2
Perfect score: 651
Sequence: 1 QVQLQQPVTELVRPGASVML...............SDYYSGMDYWGQGTSVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:　283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
PIR 80:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	490	75.3	123	2	S20646	Ig heavy chain V r
2	483.5	74.3	120	2	S41394	Ig heavy chain V r
3	476	73.1	120	2	S25175	Ig heavy chain V r
4	476	73.1	122	2	S20643	Ig heavy chain V r
5	475.5	73.0	120	2	B22769	Ig heavy chain V r
6	472	72.4	117	2	B27563	Ig heavy chain V r
7	470	72.2	138	2	E32513	Ig heavy chain pre
8	468.5	72.0	116	2	S53751	Ig heavy chain pre
9	458.5	70.4	122	2	S24287	antibody Fab Je1 1
10	458.5	70.3	139	1	MHMS18	Ig heavy chain pre
11	457.5	70.3	287	4	PC4402	pelB leader/Ig hea
12	454.5	69.8	126	2	S31930	Ig gamma chain pre
13	453.5	69.7	141	2	JL0076	Ig gamma chain pre
14	452.5	69.5	135	1	A30577	Ig heavy chain pre
15	452	69.4	138	1	HVMST7	Ig heavy chain pre
16	451	69.3	136	2	PL0208	Ig heavy chain pre
17	449	69.0	246	2	S38950	Ig heavy chain pre
18	449	69.0	446	2	S40295	Ig gamma-2a chain
19	448.5	68.9	139	2	PS0024	Ig gamma chain pre
20	448.5	68.6	118	2	C30560	Ig heavy chain V r
21	446.5	68.3	117	2	S09956	Ig heavy chain V r
22	444	68.2	138	2	S21810	Ig heavy chain V-D
23	442.5	68.0	117	2	S55541	Ig heavy chain V r
24	442.5	68.0	121	2	A39276	Ig heavy chain V r
25	442	68.0	121	2	A26405	Ig heavy chain V r
26	441	67.7	121	2	B48677	Ig heavy chain V r
27	441	67.4	123	2	PH1160	Ig heavy chain V r
28	439	67.4	98	2	S26317	Ig heavy chain V r
29	439	67.4	119	2	PL0089	Ig heavy chain V r
30	438	67.3	117	2	G45722	Ig anti-glycoprotein
31	437	67.1	136	2	B47159	Ig heavy chain V r
32	436	67.0	131	2	A27472	Ig heavy chain V r
33	435.5	66.9	139	2	A27609	Ig heavy chain pre
34	435	66.8	118	2	S38565	Ig heavy chain V-D
35	435	66.8	123	2	F48677	Ig heavy chain V r
36	434.5	66.7	116	2	S26309	Ig heavy chain V-D
37	434.5	66.7	119	2	A24672	Ig heavy chain pre
38	434	66.7	123	2	G48677	Ig heavy chain pre
39	434	66.7	140	1	HVMSG7	Ig heavy chain V r
40	433	66.4	109	2	S26318	Ig heavy chain V r
41	432.5	66.4	136	2	JL0077	Ig heavy chain V r
42	431	66.2	116	2	S55542	Ig heavy chain V r
43	430.5	66.1	123	2	S60067	Ig heavy chain V r
44	430	66.1	140	2	PH1482	Ig heavy chain V r
45	428	65.7	121	2	A21854	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S20646
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20646
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacti
A;Reference number: S20639
A;Cross-references: UNIPARC:UPI000011602O; EMBL:X55001; NID:g52612; PIDN:CAA46134.1; PID:
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-123 <LOS>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 490; DB 2; Length 123;
Best Local Similarity 78.0%; Pred. No. 3.3e-36;
Matches 96; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

```
Qy   1  QVQLQQPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPCQGLEWIGVIDPSDTYPNY   60
           ||||| |||||:|||||||:|||| ||| |||||||||||| ||||||||:|||||| |
Db   1   QVQLQPGTELVKPGASVKLSCKASGYTFTNYWIHWVKQRPGQGLEWIGEIAPSDNYTYY   60

Qy  61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYSG--MDYWGQGTSVT  118
            ||:|||||||||  ||:|||||||||||:|||:|||| ||            |||||||||||||
Db  61   NQNFKGKATLTVDKSSNTAYMQLSSLTSEDSAIYYCSRRRYYDLRRGYAMDYWGQGTSVT  120

Qy 119  VSS 121
         |||
Db 121  VSS 123
```

RESULT 2
S41394
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S41394
R;Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
A;Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN?
A;Reference number: S41393
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Cross-references: UNIPARC:UPI0000116582; EMBL:Z29586; NID:g452354; PIDN:CAA82703.1; PII

```
C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match         74.3%;   Score 483.5;   DB 2;   Length 120;
Best Local Similarity 76.6%;  Conservative  7;  Mismatches  15;  Indels  7;  Gaps  2;
Matches  95;

Qy    1  QVQLQQPGPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY   60
         ||||| |  |:||:||||||||| |  ||| ||  || |||||||||||||| ||||:|
Db    1  EVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEIDPSDSYTYY    60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYS---GMDYWGQGTSV   117
         |:||  |||||||| :||||||||||||| ||||||||||          |  || |||
Db   61  NQKFKGKATLTVDKSSSTAYMQFSSLTSEDSAVYYCARR------YYGSRVSMDYWCQGTSV 116

Qy  118  TVSS  121
         |||
Db  117  TVSS  120
```

RESULT 3
S25175
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25175
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Reference number: S25175
A;Description: Structure and binding properties of monoclonal antibodies to core histone
A;Reference number: S25174
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-120 <MON>
A;Cross-references: UNIPARC:UPI000011160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

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Matches  95;   Conservative  4;   Mismatches  18;   Indels  8;   Gaps  2;

Qy    1  QVQLQQPGPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY   60
Db    1  QVQLQQXXGAELVKPGASVKLSCKASGYTFIRYWIHHVKQRPGQGLEWIGEIDPSDNYTYY    60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYS---GMDYWGQGTSV    115
Db   61  NQKFKGRATLTVDKSSSTAYMQLSSLTSEDSAVYYCARR-----EYYDLRRGHAMDYWCQGT 117

Qy  116  SVTVS  120
Db  118  SVTVS  122
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RESULT 4
S20643
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20643
R;Losman, M.J.; Fasy, T.M.; Novick, K.E.; Monestier, M.
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20643
A;Reference number: S20639
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-122 <LOS>
A;Cross-references: UNIPARC:UPI000011601D; EMBL:X64998; NID:g52606; PIDN:CAA46131.1; PID
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match         75.0%;   Pred. No. 5.4e-35;   Mismatches 17;   Indels  0;   Gaps  0;
Best Local Similarity 90;    Conservative  13;

Qy    1  QVQLQQPGPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY   60
Db    1  QVQLQQPGAELVKPGASVMLSCKASGYTFTSYWMHWVKQRPGQGLEWIGVIDPSDSETHY    60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYISGMDYWGQGISVTVS   120
Db   61  NQKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVFYCAREKITDDYNYFDYWGQGTTLTVS   120
```

```
Query Match         73.1%;   Score 476;   DB 2;   Length 122;
Best Local Similarity 76.0%;  Pred. No. 5.5e-35;
```

```
Matches  95;   Conservative  4;   Mismatches  18;   Indels  8;   Gaps  2;

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYYS---GMDYWGQGTSV   115
Db   61  NQKFKGRATLTVDKSSSTAYMQLSSLTSEDSAVYYCARR-----EYYDLRRGHAMDYWCQGT 117

Qy  116  SVTVS  120
Db  118  SVTVS  122
```

RESULT 5
B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C;Accession: B22769
R;Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between V
A;Reference number: A90971; MUID:84236026; PMID:7188353
A;Accession: B22769
A;Molecule type: protein
A;Residues: 1-120 <DIL>
A;Cross-references: UNIPARC:UPI0001176B76
A;Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2,
A;Note: peptides and unsequenced residues were positioned by homology with the B1-8 seque
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match         73.0%;   Score 475.5;   DB 2;   Length 120;
Best Local Similarity 76.4%;  Pred. No. 6e-35;   Mismatches 15;   Indels  5;   Gaps  2;
Matches  94;   Conservative  9;

Qy    1  QVQLQQPGPVTELVRPGASVMLSCKASDYPFTNYWIHWVKQRPGQGLEWIGVIDPSDTYPNY   60
Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGVIDPSDTYPNY    60

Qy   61  NKKFKGKATLTVVSSSTAYMQLSSLTSDDSAVYYCARNGDSDYY---SGMDYWGQGTSVT   118
Db   61  NQKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARR---YDYYGSSYFDYWGQGTTLT  117
```

RESULT 6
B27563
Ig heavy chain V region (T14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
C;Accession: B27563
R;Carmack, C.E.; Pincus, S.H.
J. Immunol. 137, 3983-3989, 1986
A;Title: Variable regions of antibodies to synthetic polypeptides. II. Analysis of variab
A;Reference number: A92812; MUID:87059009; PMID:3097139
A;Accession: B27563
A;Molecule type: DNA
A;Residues: 1-117 <CAR>
A;Cross-references: UNIPARC:UPI000011CA49; GB:M14974; NID:g195260; PIDN:AAA38226.1; PID
A;Note: this sequence was determined from the differentiated gene
A;Note: the authors translated the codon GGT for residue 54 as Ala and TAC for residue 5
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;12-95/Domain: immunoglobulin homology <IMM>

```
Query Match         72.4%;   Score 471.5;   DB 2;   Length 117;
```